```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	251334 251334 261334 2723334 273334 273334 273334 273334 273334 273334 273334 273334 273334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 27334 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734 2734	linear PAT 17-JUL-2003 antigen and utilization
ΙD	manapapanananapapapanananapapapanananapapapanananapapapanananananananananananananananananananan	702 bp DNA bacterium tuberculosis 04 con,M. and Neto,A.C.
% Query e Match Length DB	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	BD251334 Fused protein of Mycothereof. BD251334. BD251334. BD251334. BD251334.1 BD251334
Result No. Score		RESULT 1 BD251334 LOCUS DEFINITION ACCESSION VERSION VERSION CETWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

ô

Gaps ò

Length 702; Indels

Reed,S.G., Skeiky,Y.A., Dillon,D.C., Alderson,M. and Campos-Neto,A. Fusion proteins of Mycobacterium tuberculosis antigens and their

AUTHORS TITLE

JOURNAL FEATURES

ORIGIN

Patent: US 6627198-A 27 30-SEP-2003; Location/Qualifiers 1. 702 /organism="unknown" /mol_type="genomic DNA"

204

240 264

180

120 144

84

1 Acescosostoceanaacticcascostocasestosescasesantoscantoceano 25 ACGGCCGCGTCCCATAACTTCCAGCTGTCCCAGGGTGGCCAGGGATTCGCCATTCCGATC GGGCAGGCGATGGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCATCAT

Query Match
100.0%; Score 396; DB 6; I
Best Local Similarity 100.0%; Pred. No. 4.5e-57;
Matches 396; Conservative 0; Mismatches 0;

241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300

265 ATCACCGCGGTCGACGCCCCCCATCACTCGGCCACCGCGATGGCGGAACGCGCTTAAC

요 8 용 ठे ď

ò

361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396

301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCT

205 GICCAACGCGTGGGTCGGGGAGCGCTCCGGCGGCAAGTCTCCGCATCTCCACCGGCGACGTG

181 GICCAACGCGIGGICGGGGGGCGCCGCGCAAGICICGGCAICICCACCGGCGACGIG

> g ð 셤

121 ATCGGGCCTACCGCCTTCCTCGGCTTTGGGTGTTGTCGACAACAACAACGGCAACGACGA

61

셤 ઠ 쉱 $\dot{\delta}$ 324 360 384

```
241 ATCACCGCGGTCGACGGCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCGGGCCTACCGCCTTCCTCGGCTTTGGGTGTTCGACAACAACGGCAAACGGCGCACGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GICCAACGCGIGGICGGAGGGGTCCGGCGCAAGICTCGGGCAICTCCCACCGGCGACGIG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 GTCCAACGCGTGGTCGTCGCGAGCGCTCCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGCCCCCGTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
(1) . (696)
(2) . .(700)
(3) . .(701) .

Location/Qualifiers
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .702
| . .703
| . .703
| . .703
| . .704
| . .704
| . .705
| . .704
| . .705
| . .705
| . .706
| . .706
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| . .707
| .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 396; DB 6;
Best Local Similarity 100.0%; Pred. No. 4.5e-57;
Matches 396; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $ A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    요
```

```
tuberculosis complex.

(bases 1 to 1068)

(dicquel,B., Portnoi,D., Lim,B., Pelicic,V., Guigueno,A. and Salmoniere,Y.G.D.L.

Sequences nuclieic acid from polypeptides exportes from mycobacteries, vector the comprenant and applications at diagnostic and the prevention from the tuberculose

Patent: JP 2002534956-A 256 22-0CT-2002;
                                     BD274032 10-1016 bp DNA linear PAT 17-JUL-2003 Sequences nuclieic acid from polypeptides exportes from mycobacteries, vector the comprenant and applications at diagnostic and the prevention from the tuberculose.
                                                                                                                                                                                          BD274032.1 GI:33083800
JP 2002534956-A/256.
Mycobacterium tuberculosis
Mycobacterium tuberculosis
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae; Mycobacteriaceae, Mycobacterium, Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OS Mycobacterium tuberculosis
PN JP 200234956-A/256
PD 22-OCT-2003
PF 14-AUG-1998 JP 2000509849
PR 14-AUG-1997 FR 97/10404,11-SEP-1997 FR 97/11325 PI
BRIGHTER GICQUEL, DENIS PORTNOI, ENG-MONG LIM, VLADIMIR PELICIC, PI
AGNES GIIGUENO, YUES GGGUET DE LA SALMONIERE
PC C12N15/09,A61K39/04,A61K48/00,A61P11/00,A61P31/04,C07K14/35,
                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
RESULT 3
BD274032
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
```

PAT 18-DEC-2003

linear

702 bp US 6627198.

AR403747 Sequence 27 from patent AR403747 AR403747.1 GI:40151423

RESULT 2
AR403747
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

Unknown. Unclassified. 1 (bases 1 to 702)

Unknown.

ORGANISM REFERENCE m

```
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1030 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGGC 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                  100.0%; Score 396; DB 6;
100.0%; Pred. No. 4.1e-57;
ive 0; Mismatches 0;
                                                                                                                           WOTKSGGTRIGNVTLAEGPPA
                                                                                                                                                                                     al Similarity 100.
396; Conservative
                                                                                                                                                                     Query Match
Best Local S:
Matches 396,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
BD274033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       유
                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                          심
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Portnoi,D. and Guigueno,A.
Polypeptide nucleic sequences exported from mycobacteria, vectors comprising same and uses for diagnosing and preventing tuberculosis Patent: WO 9909186-A 907 25-FEB-1999;
PORTNOI DENIS (FR); GUIGTENO AGNES (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               970 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGGT 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAT 24-AUG-2000
                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                            849
                                                                                                                                                                                                                                                                                                                                                                                                                                                    909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 ATCACCGCGGTCGACGCCTCCGATCAACTCGGCCACGGCGATGGCGGACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    729
                                                                                                                                                                                                                                                                                                                                                                                                                        GICCAACGCGIGGICGGGGGGGCGCGGCGAAGICICGGCAICICCACCGGCGACGIG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                               9
             М
                                                                                                                                                                                                                                                                   GGGCAGGCGATGGCGAGTCGCGGCCAGATCCGATCGGGTGGGGGGTCACCCGTTCAT
                                                                                                                                                                                                                                                                                                                                                               ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGCGT
                                                                                                                                                                                                                                              1 ACCCCCCCCCCCATAACTTCCACCTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
 CO7K16/12,
CO7K19/00,C12N1/21,C12P21/02,C12Q1/02,C12Q1/68,G01N33/50,
3/53//
                                                                                                                                                                                                                   Gaps
                                           ပ္ပ
                                         (CIZNIS/09,CIZRI:32),CIZNIS/00,(CIZNIS/00,CIZRI:32)
Key
Location/Qualifiers
Location/Qualifiers
                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                      Length 1068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .1068
/organia="Mycobacterium tuberculosis"
/mol_type="unassigned DNA"
/db_xref="taxon:1773"
                                                                                                    1. 1068
/organism="Mycobacterium tuberculosis"
/mol_type="genomic DNA"
/db_xrefe="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="unnamed protein product; 50D"
/codon start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1030 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                      100.0%; Score 396; DB 6;
larity 100.0%; Pred. No. 4.1e-57;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1068 bp
Sequence 907 from Patent WO9909186.
AX005788
AX005788.1 GI:9928795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis
Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .1068
                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 396; Conserv
                                                         Key
PC COT
GOIN33/F
PC (C)
FH Ke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                       730
                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
AX005788
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                         FEATURES
                                                                                                                                                               ORIGIN
```

d

 $\dot{\delta}$ g ð

음 참

8 B 8

g à

g

ò

```
BD274033 sequences nuclieic acid from polypeptides exportes from mycobacteriaes, vector the comprenant and applications at diagnostic and the prevention from the tuberculose.
BD274033 BD274033 BD274033.
BD274033.
BD274033.
BD274033.
BD274033.
BD274033.
AT :002534956-A/257.
Wycobacterium tuberculosis
Mycobacterium tuberculosis
Bacteria, Actinobacteria, Actinobacterides, Mycobacterines, Mycobacterium, Mycobacterium, tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases I to 1143)
Glacquel, B., Portnoi, D., Lim, E., Pelicic, V., Guigueno, A. and Salmoniere, Y.G.D.L.
Sequences nuclieic acid from polypeptides exportes from mycobacteries, vector the comprenant and applications at diagnostic and the prevention from the tuberculose and the prevention 15 2002534956-A 257 22-OCT-2002;
INSTITUT PASTEUR
/protein_id="CAC05178.1"
/db_xref="G1:9928796".
/db_xref="G1:9928796".
/db_xref="BRWTRENBL:CAC05178"
/db_xref="BRWTRENBL:CAC05178"
/td_anslation="MRNSRRESIENSWILLSYLAAVGLGLATAPAQAAPPALSQDRFAD
FPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATD
INAFSVGSQGYTGVDVVGYBRTQDIAATLGLRGAGEDFBAALGGGVAVGANGS
GQGGTPRAVPGRVVALGQTVQASDSI-TGABETLANGILQFDAAIQPGDSGGPVVNGLGG
VVGNNTPASDNPQL-SQGGQGFAIPIGAGANAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
MNGNGARVQRAVGSAPAAGTCSTGTGABETLANGILQFTAFLGLGVVD
MNGNGARVQGAPAAGTCSTGTGABTLANGILGFTAFLGLGVVD
MNGNGAPAVGARVAGAAAAGTGTGTGTGABTANGAATANADALNGHHPGDVISVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1029
                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OS Mycobacterium tuberculosis

PN JP 2002534956-A/257

PD 22-OCT-2090

PF 14-AUG-1999 FR 97/10404,11-SEP-1997 FR 97/11325 PI

BRIGITTE GICQUEL, DENIS PORTNOI, ENG-MONG LIM, VLADIMIR PELLCIC, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    670 ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGGATTCGCCATTCGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 grcchacecergercessagescreessesaherercescarercescare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              850 checaaccechechecaaccecheccacaachechectaccecarerecaccaccaccie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ATCACCGCGCTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAAACGGCGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Ö
                                                                                                                                                                                                                                                                                                                                                                   Length 1068;
```

505

protein product; SEQ ID NO

```
301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
BD251322
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       중 음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                        ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Portnoi,D. and Guigueno,A.
Polypeptide nucleic sequences exported from mycobacteria, vectors comprising same and uses for diagnosing and preventing tuberculosis Patent: WO 990918-99 25-FEB-1999;
PORTNOI DENIS (FR); GUIGUENO AGNES (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAT 24-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCGCACGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 ATCACCGCGGCGCGCGCGCTCCGATCAACTCGGCCACGCGGATGGCGGACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                            865 Arceeectracectrecteeecrreeergrangerereeacaacaacaacaacaacaacaacaacaacaacaacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCCATCTCCACCGGCGACGTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GICCAACGCGIGGICGGGAGCGCICCGGCGAAGICICGGCAICTCCACCGGGAACGIC 984
                                                                                                                                                                                                                                                                                                                           804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis
Mycobacterium tuberculosis
Bacteria; Actinobacteria, Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                                                                                                                                                                                                                                                                                                9
AGNES GUIGUENO, YVES GOGUET DE LA SALMONIERE
PC C12N15/09, A61K39/04, A61K48/00, A61P31/00, A61P31/04, C07K14/35,
PC C07K16/12,
PC C07K16/12,
PC C07K19/00, C12N1/21, C12P21/02, C12Q1/68, G01N33/50, PC
Q01N33/53/3/
PC (C12N15/09, C12R1:32), C12N15/00, (C12N15/00, C12R1:32) CC SEQ
PT Key (A1. '(1140)
                                                                                                                                                                                                                                                                                                                   1 ACGGCCGCGTCCCGATAACTICCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                       1143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                  0; Indels
                                                                                               Location/Qualifiers
(4). .(1140).
Location/Qualifiers
1. .1143
/ organism="Mycobacterium tuberculosis"
/mol_type="genomic DNA"
/db_xref="taxon:1773"
                                                                                                                                                                                                                                       Length

    .1143
/organism="Mycobacterium tuberculosis"
/mol_type="unassigned DNA"
bxref="taxon:1773"
    .1143

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                     100.0%; Score 396; DB 6;
100.0%; Pred. No. 4.1e-57;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AX005790 1143 bp
Sequence 909 from Patent WO9909186.
AX005790 AX005790.1 GI:9928797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis complex
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 396; Conserv
                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                        805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
AX005790
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWCRDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                     FEATURES
```

Dp ö

qq δ g 8 g à d ò

d ò CDS

```
BD251322.1 GI:33061092
BD251322.1 GI:33061092
JP 2002510494-A/1.
synthetic construct
artificial sequences.
1 (bases 1 to 2287)
Skeiky, Y.A.W., Alderson, M. and Neto, A.C.
Eused protein of Mycobacterium tuberculosis antigen and utilization thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BD251322 2287 bp DNA linear PAT 17-JUL-2003
Fused protein of Mycobacterium tuberculosis antigen and utilization
thereof.
/transl_table=11
/brocein_id="CACOS179.1"
/brocein_id="CACOS179.1"
/brocein_id="CACOS179.1"
/db_xref="di:9928798"
/db_xref="Ti:9928798"
/db_xref="REWINERRIBL:CACOS179"
/translation="KNPARRIBLEDEPENDINGSYCONGEOVNINTKLGYNLAN-VCIGLATAPAGAAPPALSORFPALPLDEPSAWVAQVGPQVVNINTKLGYNNAVGA
GTGIATDAPAGAAPPALSORFPALPINAFSVGSGQTYCYDVGYDRTQDVAVGLRGAG
GLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGGTVQACDSITGAEFTLN
GLIGPDAALGGGVAVGTEVVVAMGNSGGVGWNTAASDHFQLSGGGFAIPIGGAWAIAGG
IRSGGGSFTVHIGPTAFLGLGVVDNNGNATASDHFQLSGGGFAIPIGGDWITAVDGA
PINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAEGPPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1104
                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      804
                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OS Artificial Sequence
PN UP 200210494-A/1
PD 200210494-A/1
PD 09-APR-2002
PF 07-APR-1999 JP 2000542460
PR 07-APR-1999 US 09/056556,30-DEC-1998 US 09/223040 PI
YASIR A W SKEIKY,MARK ALDERSON,ANTONIO CAMPOS NETO PC
CL2N15/09,A6TK39/04,A6TK48/00,A6TP31/04,CO7K14/35,CO7K19/00, PC
CL2P21/02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              925 GICCAACGCGIGGICGAGGAGCGCTCCGGCGGCAAGICTCGGCATCTCCACCGGCGACGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGAACGCGCTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ATCGGGCCTACCGCCTTCCTCGGCTTGTCGACACAACGGCAACGCCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       865 AICGGGCCTACCCCTCCTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGACGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 Greenacacaracacaracacacacacacacana arteracacacana and anacaracana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               805 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGGTCACCGACGGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACGGCCGCGTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGAATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GGGCAGGCGATGGCGATCGCGGGCCAAGATCCGATCGGGTGGGGGGTCACCCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 4.1e-57;
Matches 396; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1105 ACAGGGAACGTGACATTGGCCGAGGAACCCCCGGCC 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 ACAGGGAACGTGACATTGGCCGAGGGACCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent: JP 2002510494-A 1 09-APR-2002;
CORIXA CORP
```

us-09-684-215b-3.rge

Duery Match 100.0%; Score 396; DB 6; Length 2287; 4atches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGAGGAATCGCCATTCCGATC 3 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGAGGAATCGCCATTCCGATC 61 GGCCAGGCGATCGCCGGCCCAATCCGAGGTGAGGAGGAATCGCCATTCAT 123 GGCCAGCCATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCACC	Db 243 GTCCAACGCGTGGAGGCGCTCCGGGGGAAGTCTCGGCGATCTCCACCGGCGATCTCGCGCGATCGTCGCGGATCGTCGCGGATCGTCGCGGATCGTCGCGGATCGTCGCGGTTAAC 300 Qy 241 ATCACCGGGGTCGACGGCGTCCGATCAACTCGGCCACCGCGATGGCGGACGCGTTAAC 300 Db 303 ATCACCGGGGTCGACCGCTCCGATCAACTCGGCCATGGCGGAGCGCGCTTAAC 362 Qy 301 GGCATCATCCCGGTGATCTCCGGTGACCTGCAAGTCGGGGGCGCGCGT 422 Db 363 ACAGGGAACGTGACGATCTCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCGC		NEFERENCE 1 (Joses I 10 224). NEFERENCE 1 (Joses I 10 224). AUTHORS Red(AS.G., Skeiky,Y.A., Dillon,D.C., Alderson,M. and Campos-Neto,A. TITLE Pation proteins of Mycobacterium tuberculosis antigens and their uses JOURNAL Patent: US 6627198-A 1 30-SEP-2003; FEATURES 12287 //organism="unknown" //mol_type="genomic DNA"	Query Match 100.0%; Score 396; DB 6; Length 2287; Best Local Similarity 100.0%; Pred. No. 3.6e-57; O; Gaps O; Matches 396; Conservative O; Mismatches O; Indels O; Gaps O; Oy 63 ACGGCGCGTCCGATAACTTCCAGCTGCTCAGCAGGATTCGCCATTCCGATC 122 GGGCAGCGTCCGATAACTTCCAGCTGCTCAGGATTCGCCATTCCGATTCTCATC 122 Oy 61 GGGCAGCGATGGCGATCGCGGAGTCCAGATCCGGTCGCCATCATCAT 182 Oy 123 GGGCAGCGATGGCGATGGCGGATGGGGTGGGGGGGGCACCCCCCCC
PC C12N15/00 CC Description of Artificial Sequence:tri-fusion protein Ra12- CC TDH9-Ra35 CC (designated Mb32A) CC n = g, a, c or t FT modified base (30) FT cbs (42). (2231) FT modified base (270). FT cbs (42). (2231) FT cbs (42). (2231) FT modified base (270). FM modified base (32) FT modified base (32) FT cbs (42). (2231) FT cbs (42). (2231) FT modified base (220). FT modified base (220). FT modified base (320).	y Match Local Similarity 100.0%; Fred. No. 3.6e-57; hes 396; Conservative 0; Mismatches 0; Indels 0; Gaps 1 ACGGCCGCGTCCCGATACTTCCAGCTGTCCCAGCGGGGATTCGCCATTCCGATC	121 ATCGGGCCTACCTCGGCTTGGGTTGTGGACAACAGGAACAGGGGGCGCGCGAACGGGGGCCCGGGAACGGGGCCCCGGAACGGGGCCCCGGAACGGGCCCCGGAACGGCCAACGGCCAACGGCCCACGAACGGCCAACGGCCAACGGCCACGAACGGCCACGAACGGCCACGAACGCCACGAACGCCACGAACGCCACGAACGCCACGAACGCCACGAACGCCACGAACGCCACGAACGCCACGAACGCCACGAACGCCACGAACGCCACGAACGCCACGAACGCCAACGCCAACGCCAACGCCAACGCCAACGCAACGCCAACGCAACGCCAACGCAACGCCAACGCAACGCCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACACAACA	QV 301 GGGGATCATCCCGGTGACCTCGGGAAACCAAGTCGGGGGACGCGT 360 Db 363 GGGCATCATCCCGGTGACCTCGGCAAACCAAGTCGGGCGACGCT 422 QV 361 ACAGGGAACGTGACGTCTCCGGGACCCCGGCC 396 Db 423 ACAGGGAACGTGACTTGGCCGAGGGACCCCCGGCC 396 Db 423 ACAGGGAACGTCAATTGGCCGAGGGACCCCCGGCC 458 RESULT 8	AR303127 AR303127 AR303127 BENINTION Sequence 1 from patent US 6544522. ACCESSION AR303127

```
gene
                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="MGEFDFKLRFAQSPVARLATSTPDGTPHLVPVVFALGARRPAEA
TRADVIYTPARKKTTQFKREALANLEENPRASVLVDSYADDWTQLWWVRADGVAAIH
RDGSVWRAAYRLLEAKYTQYGSVPLNGPVIALAVQRWASRHA"
COMPLEMENT (643. . 1062)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A linear BCT 27-APR-2001 section 11 of 280 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis CDC1551
Mycobacterium tuberculosis CDC1551
Mycobacterium tuberculosis CDC1551
Bacteria, Actinobacteria, Actinobacterium;
Corynabacterinaee, Mycobacteriaceae, Mycobacterium;
tuberculosis complex.
1 (bases 1 to 14029)
1 (bases 1 to 14029)
1 (bases 1 to 14029)
1 (bases 2 to 14029)
1 (bases 3 to 1402
241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
                                                    303 ATCACCGCGCTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGTTAAC 362
                                                                                                                                             301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
                                                                                                                                                                                                  [Joses 1 to 14029]
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Reterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gill,J., Mikula,A. and brown,...

Direct Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
Location/Qualifiers

    14029 / Arganism="Mycobacterium tuberculosis CDC1551"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tocome identified by Glimmer2; putative"

codon start=1
(trans] table=11

product="hypothetical protein"

protein id="AAK4353.1"

db_xref="G1:13879611"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                           361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                    423 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/trans1_table=11
/product="hypothetical_protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE006925 14029 bp D
Mycobacterium tuberculosis CDC1551,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="CDC1551"
/D_xref="taxon:8331"
/note="clinical strain"
complement(99. 533)
/gene="MT0129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (643. .1062)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (99, .533)
/gene="MT0129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete genome.
AE006925 AE000516
AE006925.1 GI:13879610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE006925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                           ò
                                                            셤
                                                                                                                                         ò
                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                    g
```

```
/transI_table=11
/product="DNA-binding protein, CopG family"
/protein_id="AAK44355.1"
/db_xref="GI:13879613"
/translation="MTKKPRNPADYVIGDDVEVSDVDLKQEEVYVDGERLTDERVEQM
/translation="MTKKPRNPADYVIGDDVEVSDVDLKQEEVYVDGERLTDERVEQM
ASSELRLAREREANLIPGGGSLSGGSAHSPAVQVVVSKATHAKLKELARSRKMSVSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="serine protease, putative"
/protein id="pakk4357.1"
/protein id="pakk4357.1"
/protein id="pakk4357.1"
/db.xref="d1:13879512"
/translation="wasnsrrsslarkswildsvilahavglochapappalesODRFAD
FPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATD
FPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATD
FPALPLDPSAMVGVVVQVQYPRTQDVAVLGYRGGGGEPVVNGLGQ
GQGTPRAVPGRVVALGQTVQASDSLITGABETLNGILQPDAAIQPGDSGGPVVNGLGQ
VVGMNTAASDNFQLSGGGGGPPTPLGGAMALAGQTRSGGGSPTVHICPTAFLGIGVVD
NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transI_table=11
/prduct=*alpha-amylase family protein"
/protein.id="ARK4358.1"
/db_xref="GI:13879616"
/db_xref="GI:13879616"
/db_xref="GI:13879616"
/db_xref="GI:13879616"
/db_xref="GI:13879616"
/db_xref="GI:13879616"
/db_xref="GI:13879616"
/db_xref="GI:13879616"
/db_xref="GI:1081061"

/protein_id="AAK44354.1"
/db_xref="G1:13879512"
/translat.con="WASSSSELPLEHCVSDDQVTVVGFDGDDLGKTARRIAALVVQRA
/franslat.con="WASSSSELPLEHCSSPRDPDFLHASSMYSILGMCQSVNGRPFDAIA
LVSVRLCHVQTDPTDSCGGRDRPGQLPCAPLDYHRHH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDYYVWSDTSERYTDARIIFVDTEESNWSFDPYRROFYWRREFSHOPDLNYDNDAVOE
AMIDVIRFWLGLGIDGFRLDAVPYLFEREGTNCENLDETHAFLKRVRKVVDDEFPGRV
LLAEANQWPGDVVEYFGDFNTGGDECHMAFHPPLMPRIFWAVRRESRFPISEIIAQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to GB:AL123456; identified by sequence similarity; putative" /codon start=1 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4695. .6500
/gene=nWT0134"
4695. .6500
/gene=nWT0134"
/note="similar to GP:2808807; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="identified by match to protein family HMM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="identified by match to protein family HMM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WQTKSGGTRTGNVTLAEGPPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity; putative"
/codon_start≈1
/transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRPVLDEFVQRETGRILPRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1682, .3367
/gene="MT0132"
1682, .3367
/gene="MT0132"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3519. .4586
/gene="MT0133"
3519. .4586
/gene="MT0133"
                                                                                                                                                                                                                                                                                                           gene="MT0131"
                                                                                                                                                                                                                                                                                                                                                           1047. .1415
/gene="MT0131"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon start=1
transI table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon start=1
transI table=
```

us-09-684-215b-3.rge

```
/product="hypothetical protein"
/product="hypothetical protein"
/protein_id="AAK44360.1"
/protein_id="100.18"
/pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="esterate, putative, antigen 85-C"
/protein_id="AaK44361.1"
/protein_id="AaK44361.1"
/protein_id="AaK44361.1"
/protein_id="Garase, putative, antigen 85-C"
/protein_id="Garase, putative, post of the protein and pro
PIPDMAQWGIFLRNHDELTLEMVTDEERDYMYAEYAKDPRMKANVGIRRRLAPLLDND
ROYZELFTALLLISLEGSPVLYGDETGMGDYIMLGRRDGYRIEMOWFPDRNAGFSTAN
PGRLYLPPRQDPYGYQANVURAQRDTSTSLLNFTRTMLAVRRHPAPAVGAFQELGG
SNPSYLLAYMQQVAGDGDTYLCVNNLSRFPOPIELDLGQWTNYTPVELTGHVEFPRIG
QVPYLLITLPGHGFYWFQLTTHEVGAPPTCGGERRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MT0138"
/note="similar to SP:P08634 PID:46222; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="similar to GP:2808801; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="WT0137" to SP:P31953 GB:X57229 PID:48828 /note="similar to SP:P31953 GB:X57229 PID:48828 pib:1567734 PID:187254; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="nodulation protein N-related protein"

'protein.id="ARK44362.1"

Da xref="G1:13879620"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence similarity; putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (8949, .9989)
/gene="MT0137"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (8949. .9989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity, putative"
/codon start=1
/trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MT0136"
8038. .8817
/gene="MT0136"
                                                                                                                                                                                                                                                                                                                                      6603. .7970
/gene="MT0135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MT0138"
10218. .10673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="MT0135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATPPAAPAAPAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .8817
                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
```

Score 396; DB 1; Length 14029; Pred. No. 2.5e-57;

100.0%;

Query Match Best Local Similarity

```
PUBMED, 9534230.

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Ezglmesez K., Gas S., Barry III C.E., Tekaia F., Badcock K., Basham D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajadream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX842572; ALO21427; ALO21428; ALO21926; ALO21927; ALO21928; ALO21929; ALO21930; ALI23456; Z74410; Z80233; Z80775; Z86089; Z92669; Z92770; Z96071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Camus J.C., Pryor M.J., Medigue C., Cole S.T.;
"Re-annotation of the genome sequence of Mycobacterium tuberculosis H37Rv";
Microbiology 148:2967-2973(2002).
                                                                                                                                      4307
                                                                                                                                                                                                                                                                              4427
                                                                                                                                                                                                                                                                                                                                                  4487
   ö
                                                                                                                                                                                                           4308 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCAACGGCGCGCGACGA 4367
                                                                                                                                                                                                                                                                                                                                                                                                                    4488 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGCGT 4547
                                                                                                                                                                                                                                            240
                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                300
                                                                                                                                                                                                                                                                                                                                                                                    360
                                 9
                                                                   4188 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                      181 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                   4428 ATCACCGCGCTCGACGGCGCTCCGATCAACTCGGCCACCCGCGATGGCGGACGCGCTTAAC
                                                                                                                                                                                                                                                                                                                                                                                    301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGT
                                   1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCGATC
                                                                                                    241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex; Mycobacterium tuberculosis.
   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis H37Rv complete genome; segment 1/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; circular genomic DNA; PRO; 341957 BP.
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 77, Created)
(Rel. 77, Last updated, Version 1)
 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome sequence";
Nature 393:537-544(1998).
   Matches 396; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 98295987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBMED; 12368430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-NOV-2003
21-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX842572.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BX842572
                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z97050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX842572
                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                    g
                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                     à
                                                                                                                                                                         ਨੇ
                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                ઠે
```

```
1-341957
Parkhill J.;
       source
      Key
```

```
/evidence=EXPERIMENTAL
/notes=RV0003, (MTCY10H4.01), len: 385 aa. recF, DNA
/notes=Rv0003, (MTCY10H4.01), len: 385 aa. recF, DNA
replication and repair protein (see citations below),
equivalent to others Mycobacterial DNA replication and
repair proteins e.g. NP 301131.1|NC 002677 from
Mycobacterium leprae (185 aa); 0917518REF MYCPA from
Mycobacterium avium subsp. paratuberculosis (186 aa);
P5016|RECF MYCSM from Mycobacterium smegmatis (384 aa);
P5016|RECF MYCSM from Mycobacterium smegmatis (384 aa);
P5016|RECF MYCSM from Mycobacterium smegmatis (384 aa);
P5016|RECF MYCSM from Listeria in Streptomyces
coelicolor (373 aa); NP 440892.1|NC 000911 from
Syncehocystis sp. strain PCC 6603 (384 aa);
NP 469352.1|NC 00312 from Listeria innocua (370 aa); etc.
Contains PS00017 AEP/GTP-binding site motif A (P-loop),
PS00617 RecF protein signature 1, and PS00618 RecF protein
signature 2. BELONGS TO THE RECF FAMILY."
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /jocus tagg"RV0002"
/product="DNA POLYMERASE III (BETA CHAIN) DNAN (DNA MOTOGUE="DNA POLYMERASE III (BETA CHAIN) DNAN (DNA MOTOGUE="DNA POLYMERASE III (BETA CHAIN) DNAN (DNA MOTOGUE="DNA POLYMERASE")"
/prodein id="CAA16239.1"
/protein id="CAA1623
(beta chain) (EC 2.7.7.7) (see citations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tocus tag="Rv0003"
product="DNA REPLICATION AND REPAIR PROTEIN RECF
(SINGLE-STRAND DNA BINDING PROTEIN)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="dnaN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="recF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .4437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
      /note="Revool," (MT001, MTV029.01, P49993), len: 507 aa. dnaA, chromosomal replication initiator protein (see citations below), equivalent to other Mycobacterial CHROMOSOMAL REPLICATION INITIATOR PROTEINS e.g. CHROMOSOMAL REPLICATION INITIATOR PROTEINS e.g. P46388 DNAA MYCDA from Mycobacterium leprae (502 aa); P46388 DNAA MYCDA from Mycobacterium paratuberculosis (509 aa); P49992 DNAA MYCDA from Mycobacterium meegmatis (504 aa); P49992 DNAA MYCDA from Mycobacterium sucium (508 aa); P49992 DNAA MYCDA from Mycobacterium sucium (504 aa); P49992 DNAA MYCDA from Mycobacterium sucium (608 aa); P49992 DNAA MYCDA from Mycobacterium sucium (608 aa); P69992 DNAA STRRE from Mycobacterium sucium (643 aa); OSZH76 DNAA STRRE from Streptomyces reticuli (643 aa); DNAA ECOLI P03004 B3702 chromosomal replication initiator protein from Escherichia coli strain K12 (467 aa); PASTA soverlap); etc. Contains PS00017 ATP/GTP-binding site motif A (P-loop) and PS01008 DNAA protein signature. BELONGS TO THE DNAA FAMILY. Note that the first base of this gene has been taken as base 1 of the Mycobacterium tuberculosis H37RV genomic sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="PLAYS AN IMPORTANT ROLE IN THE INITIATION AND REGULATION OF CHROMOSOMAL REPLICATION. BINDS TO THE ORIGIN OF REPLICATION; IT BINDS SPECIFICALLY DOUBLE-STRANDED DNA AT A 9 BP CONSENSUS (DNAA BOX): 5'-TTATC(C/A)A(C/A)A-3'. DNAA BINDS TO APP AND TO ACIDIC PHOSPHOLIPIDS. DNAA PROTEIN BINDS THE ORIGIN OF REPLICATION (OriC), ATP AND ADP, AND EXHIBITED WEAK ATPASE ACTIVITY."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="CHROMOSOWAL REPLICATION INITIATOR PROTEIN DNAA"
/protein_id="CAA16238.1"
/protein_id="MTDDGGGFTTVWNAVVSELNGDPKVDDGPSSDANLSAPLTPQQR
AMINAVQPLINGARLLGVPSSFVQNEISERHLAAPITDALSREUGHQUQLGVRIAPPA
TDEADDTTVPPSENPATISPDTTTDNDEIDDSAAARGDNQHSWPSYFTERPHNTDSATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYAORLFPCHRVKVYSTEEFTNDFINSLRDDRKVAFKRSYRDVDVLLVDDIQFIEGKEG
IQEEFFHTFNTLHNANKQIVISSDRPPKQLATLEDRLATRFEWGLITDVQPPELETRIA
ILRKKAQMERLAVPDDVLELIASSIERNIRELEGALIRVTAFERASLMKTPFDKALABIVL
RDLIADANIMQISAATIMAATAEYFDTVEELEGPGKTRALAQSRQIAMYLCRELTDLS
LPKIGQAFGRDHTTVMYAQRKILSEMAERREVFDHVKELTTRIRQRSKR"
622. 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVTSLNRRYTFDTFVIGASNRFAHAAALAIAEAPARAYNPLFIWGESGLGKTHLLHAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2052. 3260
(evidence=EXPERIMENTAL
/note="Rv0002, (MTV029.02, MTCY10H4.0), len: 402 aa. dnaN,
                                                                                                                         Submitted (11-JUN-1998) to the EMBL/GenBank/DDBJ databases.
Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinkton, Cambridge CBHO ISA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db xref="taxon:8332"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/organism="Mycobacterium tuberculosis H37Rv"
/etrain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                            Notes:
Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1384. .1440
/note="PS01008 DnaA protein signature"
2052. .3260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . . .1524
/evidence=EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      locus_tag="Rv0001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="dnaA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
```

```
/gene="Mina" |
//gene="Mina" |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Jocus tag="MD0002"
/Jocus tag="MD0002"
/EC_number="2.7.7.7"
/note="MD0002, dnaN, len: 402 aa. Equivalent to Rv0002,
len: 402 aa, from Mycobacterium tuberculosis strain H37Rv,
199. 8% identify in 402 aa overlap). dnaN, DNA polymerase
III (beta chain) (EC 2.7.7.7) (see citations below).
III (beta chain) (EC 2.7.7.7) (see citations below).
CHAIN e.g. NP 201130 i] NC 002677 from Mycobacterium leprae subsp. paratuberculosis (399 aa); P52851 | DP3B_MYCSM from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / LTAINSTACT ON THE TOTAL TOWNS TO THE TOTAL STREAM TO THE THE TOTAL STREAM TO THE TOTAL STREAM THE TOTAL STREAM TO THE TOTAL 
Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire Bacterienne Institut Pasteur 28, rue du Dr Roux 75724 PARIS cedex 15, France. e-mail:tgarnier@asteur.fr Submitted on behalf of the Mycobacterium bovis sequencing teams, TB Research Group, Veterinary Laboratories Agency Weybridge, Woodham Lane, New Haw,Addlestone, Surrey KT15 3NB, UK. Sanger Centre, Wellcome Trust Genome Campus, Hinxton,Cambridge CB10 15A, UK. PT4 Annotation, Genopole, Institut basteur, 28 Rue du Docteur Roux, 75724 Paris Cedex 15, France. Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=experimental
/transl_table=11
/product= CHROMSOMAL REPLICATION INITIATOR PROTEIN DNAA"
/protein_id="CAD92863.1"
/db_xref="GI:31616763"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mycobacterium bovis subsp. bovis AF2122/97"
|mol_type="genomic DNA"
/strain="AF2122/97"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:233413"
L. _1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus_tag="Mb0002"
2052. .3260
/gene="dnaN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 locus_tag="Mb0001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1052. .3260
/gene="dnaN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="dnaA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="dnaA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCO
                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151817 Acedecedesteceanaactreceaetereceaegeseedeearteecarreceare 151876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151997 drcchacecerderedadecerrecesesesarereresesareresesareres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garnier,T., Eiglmeier,K., Camus,J.-C., Medina,N., Mansoor,H.,
Pryor,M., Duthoy,S., Grondin,S., Lacroix,C., Monsempe,C., Simon,S.,
Harris,B., Atkin,R., Doggett,J., Mayes,R., Keating,L.,
Wheeler,P.R., Parkhill,J., Barrell,B.G., Cole,S.T., Gordon,S.V. and
                                                                                                                                              434. .4997

fevidence=EXPERIMENTAL
/note=TRO004, (MTCY10H4.02), len: 187 aa. Conserved
/note=TR0004, (MTCY10H4.02), len: 187 aa. Conserved
hypotherical protein (see Salazar et al., 1996), highly
similar, but longer 21 aa in N-terminus, to
AAF33696.1|AF222789 unknown protein from Mycobacterium
avium subsp. paratuberculosis (166 aa); and highly similar
to NP 301132.1|NC 002677 conserved hypothetical protein
from Mycobacterium leprae (189 aa); 570990 hypothetical
protein from Mycobacterium smeqmatis (194 aa). Also highly
similar, except in N-terminal part, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX248334 11-JUN-2003 Ayoobacterium bovis subsp. bovis AF2122/97 complete genome; segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX248334 BX248333
BX248334.1 GI:31616762
Complete genome.
Mycobacterium bovis subsp. bovis AF2122/97
Mycobacterium bovis subsp. bovis AF2122/97
Mycobacterium bovis subsp. bovis AF2122/97
Corymebacterines; Actinobacteria; Actinobacteria; Actinobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCCACCGTTCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ATCACCGCGGTCGACGCCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152057 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACGGCGATGGCGGACGCGCTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCCAACGCGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCCACGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACGGCCGCGTCCGATACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 396; DB 15; Length 341957; 100.0%; Pred. No. 1.4e-57; ive 0; Mismatches 0; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The complete genome sequence of Mycobacterium bovis Online Publication PNAS 10.1073/pnas.1130426100 ( Microbiology ) 2 (bases 1 to 343050)
                                                                               4243. .4296
/note="PS00618 RecF protein signature 2"
                                 /note="PS00617 RecF protein signature 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
Les 396; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hewinson, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garnier,
                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
REMARK
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
BX248334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \delta
                                         8
```

```
Wycobactrium sengenitis (1979 an); etc. Also highly similar to others a grapholipus grammar to others a grapholipus grammar to others a grapholipus grammar to others a grapholipus manners and the grammar to other a grapholipus manners and the grammar to other a grapholipus manners and the grammar to other and the grapholipus manners and
```

gene

CDS

gene

CDS

```
152248 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACGCGATGGCGGGACGCGCTTAAC 152307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152188 GTCCAACGCGTGGTCGCGAACGCTCCCGGCAACTCTCGGCATCTCCACCGCGACGTG 152247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152008 Accecceccarceanaetrecaetrereceascaesaesaesaesaesantescaritecant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-terminal part of P35925 | YREG_STRCO HYPOTHETICAL 19.8 KDA PROTEIN (IN RECF-GYRE INTERCENIC REGION) from Streptomyces coelicolor (190 aa), FASTA scores: opt: 404, E(): 3.9e-18, (40.7% identity in 189 aa overlap)."

/codon start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=wh00005, gyrB, len: 714 aa. Equivalent to Rv0005, len: 714 aa. from Mycobacterium tuberculosis strain H37Rv, (99.9% identity in 714 aa overlap). gyrB, DNA gyrash (99.9% identity in 714 aa overlap). gyrB, DNA gyrash (99.9% identity in 714 aa overlap). gyrB, DNA gyrash (99.9% identity in 714 aa overlap). gyrB, DNA gyrash (90.0% identity in N-terminus, to other Mycobacterial DNA GYRASES GOBININI B e.g. T10005 from Mycobacterium leprae (697 aa); Q91713 [GYRB MYCRA from Mycobacterium avium subsp. paratubercullosis (677 aa) (has its N-terminus shorter); persisjegvrB MYCSM from Mycobacterium smegmatis (675 aa); etc. Also highly similar to others e.g. T10969 from Streptomyces coelicolor (686 aa); P50075 [GYRS_STRSH from
                                                                                                                                                                                                                                                                                              /rransi_rable=11
product="CONSERVED HYPOTHETICAL PROTEIN"
product="CONSERVED"
protein 1d="Cad92866.1"
db xref="G1:31616"6"
/translation="MTGSVDRPDQNRGERLMKSPGLDLVRRTLDEARAARARAGQDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAT 17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGRVASVASGRVAGRRRSWSGPGPDIRDPQPLGKAARELAKGGWSVRVAEGMVLGOM
SAVVGHQIALHARPTALNDGYLSVIAESTAMATQLRIMQAQLLAKIAAAVGNDVVRSL
KITGPAAPSWRKGPRHIAGRGPRDTYG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152068 dadchaddcantddcantdcadadatccantcadatcadagacatchccchccattan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCCAACGCGTGGGAAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ATCACCGCGCTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 geschichicocesich centratorices sanctise caractaractes contratorices contratorices and the contratorices of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGACGCGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 343050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152368 Acaddaacdreacarradcocdaddaccoccoccocco 152403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 396; DB 1;
100.0%; Pred. No. 1.4e-57;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AR169152 477 bp
Sequence 4 from patent US 6290969.
AR169152 GI:17906927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /locus_tag="Mb0005"
/EC_number="5.99.1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5123. .7267
/gene="gyrB"
/locua_tag="Mb0005"
5123. .7267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="gyrB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 396; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
AR169152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

180 190 240 250 300 310 360 370

120 130

70

```
PAT 20-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCAACGGCGCACGA
                                                                                                                                                                                                                           251 ATCACCGGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCCAACGCGTGGTCGGGAGCGCTCCGGCGACGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCACCGCGGTCGACGCCCCCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                ATCGGGCCTACCGCCTTCGGCTTTGGTTGTCGACAACGGCAAACGGCGCACGA
                                                                                                                                                                                erccaacecercesascecrccescescascrcrcescascarcrcescarcrcescescescesce
                                                                                                                                                                                                            ATCACCGCGCTCGACGCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                                                                                                                                                                   GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGCGT
                                                                                                                                                                                                                                                                                1 ACGGCCCCCCCGATAACTTCCAGCTGTCCCAGGCAGGCATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 Arcessecracescrrecresserressreresacaacaacaacaaceaceseses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grechaceceregreegeagecerrecegescaagreresecarecacegesacere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 ATCACCGCGGTCGACGCCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
11 ACGGCCGCGTCCCATACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                          GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillon,D.C.
the prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 394.4; DB 6;
Pred. No. 9e-57;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                           371 ACAGGAACGTGACATTGGCCGAGGACCCCCGGCC 406
                                                                                                                                                                                                                                                                                                                        361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Untown.

Unknown.

Unclassified.

E 1 (bases 1 to 447)

Reed, S.G., Skeiky, Y.A.W. and Dillon, D.C.

Compositions and methods for the prever tuberculosis infection

NAL Patent: US 6350456-A 4 26-FEB-2002;

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .447
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                     AR194825
AR194825
AR194825.1 GI:20244262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.7%;
Matches 395; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
                                                                                                                            131
                                                                                                                                                        181
                                                                                                                                                                                   191
                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                    301
                                          61
                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
AR194825
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                 જે
                                                                                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                     ठ
                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                   ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM Unknown.

Unclassified.

I (bases 1 to 447)

Reed, S.G., Skeiky, Y.A. W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S. and Twardzik, D.R.

Compounds and methods for diagnosis of tuberculosis

Compounds and methods for diagnosis of tuberculosis

Location/Qualifiers

1. 447

Jurce /organism="unknown"
/mol_type="unassigned DNA"
Unknown.

Unclassified.

Unclassified.

In (bases 1 to 447)

RS Reed,S.G., Skeiky,Y.A.W., Dillon,D.C., Campos-Neto,A., Houghton,R., Vedvick,T.S. and Twardzik,D.R.

Compounds and methods for immunotherapy and diagnosis of tuberculosis

The patent: US 6290869-A 18-SEP-2001;

Location/Qualifiers

Ource

//organism="unknown"
//mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAT 20-APR-2002
                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                            190
                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCCAACGCGTGGGTCGGGAGCGCTCCGGCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCACCGCGGTCGACGCCTTCGGTTCAACTCGGCCACGCGATGGCGGACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGGCACGCGT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 Arcaccecedreacececrecearcaacresseaceaceaceacearesegacecerraac 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCGT 360
                                                                                                                                                                                                                                                                               70
                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                   1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                          11 ACGGCCGCGTCCGATAACTTCCCAGCTGTCCCAGGGTGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                               GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCACGGTTCAT
                                                                                                                                                                                                                                                                                                                                                                    ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                          GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                       1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 447;
                                                                                                                                                                                                   Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 406
                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.6%; Score 394.4; DB Best Local Similarity 99.7%; Pred. No. 9e-57; Matches 395; Conservative 0; Mismatches
                                                                                                                                                                                                Score 394.4; DB Pred. No. 9e-57; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AR182442 47 bp
AR182442 47 dI:20225649
                                                                                                                                                                                                99.6%;
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 395; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371
                                                                                                                                                                                                                                                                                                                                                                                               131
                                                                                                                                                                                                                                                                                                                                                                                                                                                    191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                        71
                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
AR182442
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                  source
     ORGANISM
                                REFERENCE
AUTHORS
                                                                                                   JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                          DRIGIN
                                                                                                                                                                                                                                                                                                                                  면
다 상
다
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                           ठे
                                                                                                                                                                                                                                                                                                                                                                                                                       \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                            8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     음 강
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                          Š
```

ö

Σ̈́

60 70

130 120

180 190 240 250 300 310

1 (bases 1 to 447) inidentified unidentified unclassified. 241 RESULT 18
AX429596
LOCUS
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
SOURCE
ORGANISM source REFERENCE AUTHORS JOURNAL JOURNAL AUTHORS REFERENCE FEATURES FEATURES TITLE TITLE ORIGIN ORIGIN В g 8 8 g ઠે යි යි ઠે g ò ò Unknown.
Unclassified.
I (bases if the the theology of the the ö PAT 17-AUG-2003 20-DEC-2002 71 GGGCAGGCGATGGCGATCGCGGGCCAGATCGGGTGGGGGGGTCACCCACGGTTCAT 130 131 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCGCACGA 190 181 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGACATCTCGGCATCTCCACCGGCGACGTG 240 241 ATCACCGCGGTCGACGCCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGCT 360 70 11 ACGGCCCCCCCCCCATACTTCCAGCTCTCCCAGGGTGGCAGGATTCGCCATTCCCATC 191 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAACTCTCGGCATCTCCACCGGCGACGTG 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGACGTCGT 1 ACGCCCCCCCCATAACTICCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC Gaps ö PAT Length 447; 1; Indels Query Match 99.6%; Score 394.4; DB 6; Best Local Similarity 99.7%; Pred. No. 9e-57; Matches 395; Conservative 0; Mismatches 1; ACAGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 406 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 371 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 406 AR353302 417 bp Sequence 4 from patent US 6592877. AR353302. GI:33759108 447 bp 4 from patent US 6458366. 1. .447 /organism="unknown" /wol_type="genomic DNA" AR233097 Sequence 4 from patent 1 AR233097 AR233097.1 GI:27275533 Unknown. Unclassified. Unknown. Unknown. 361 RESULT 17
AR353302
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM AR233097 LOCUS DEFINITION ACCESSION VERSION SOURCE SOURCE ORGANISM

TITLE JOURNAL

FEATURES

ORIGIN

Бb

g

ద ò g δ

ö

qq ò Db à

 δ

REFERENCE AUTHORS

20.00.00

HOII MAY

g ò d

```
Reed, S.G., Skeiky, Y.A., Dillon, D.C., Campos-Neto, A., Houghton, R.L., Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for immunotherapy and diagnosis of tuberculosis PP 12092 patent: EP 1203817-A 4 08-MAY-2002;
CORIXA CORPORATION (US)
Location/Qualifiers
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-2002
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                       251 ATCACCGGGTCGACGGCTCCGATCAACTCGGCCACGCGGATGGCGGGATGAAC 310
                                                                                                                                                                                                                                                                                                                                             130
                                                                                                                                                                                                                                                                                                                                                                                                          190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCCACCGCGATGGCGGAACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
                                                                                                                                                                                                                                                                    70
                                                                                                                                                                                                                                                                   11 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGAATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                             311 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCACGCGCT
                                                                                                                                                                                                                                                                                                                              1 ACGCCCCCCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                 Query Match 99.6%; Score 394.4; DB 6; Length 447; Best Local Similarity 99.7%; Pred. No. 9e-57; Matches 395; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 99.6%; Score 394.4; DB 6; Best Local Similarity 99.7%; Pred. No. 9e-57; Matches 395; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .447
/organtsm="unidentified"
/mol_type="unassigned_DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AX429596 4 from Patent EP1203817.
AX429596 4 displayed AX429596.1 displayed
```

```
180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gescaesecangescancesesectacancesanceseneseseseraceceaecentear 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08/818111 PI
ANTONIO CAMPOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ပ္ပ
                         310
                                                                                                                                                                                                                                                                                                                                                                                                                                            SM unidentified

unclassified.

I (bases 1 to 447)

Read, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.S., Twardzik, D.R. and Lodes, M.J.

Compounds and methods for diagnosis of Tuberculosis

Corixa CORP

CORIXA CORP

CORIXA CORP

CORIXA CORP

PD 16-JAN-2001,
PP 01-JAN-2001

PP 07-OCT-1997 JP 1998518432

PR 11-OCT-1996 US 08/725622, 13-MAR-1997 US 08/818111 PI

STEWEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, PI ANTONIO CAMPOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PI RAYMOND HOUGHTON, THOMAS S VEDVICK, DANIEL R TWARDZIK, PI MICHAEL J LODES
OF CLYDIS/31, COTK14/35, COTK16/12, C12Q1/68, C12N15/62, G01N33/53
Strandedness: Single;
C Topology: Linear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GICCLAACGCGIGGICGGGGGGGCGCCGGGGAAGICTCGGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

99.6%; Score 394.4; DB 6; Length 447;

Best Local Similarity 99.7%; Pred. No. 9e-57;

Matches 395; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                         BD006325
Compounds and methods for diagnosis of Tuberculosis.
BD006325
BD006325.1 GI:18634696
JP 2001500383-A/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCCGGCC 396
                                                                                                                                                                                    371 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .447
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PI RAYN
MICHAEL J
PC C12N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191
                                                                          301
                                251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
source
                                                                                                                                                                                                                                                                        RESULT 20
BD006325
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 & 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                음
장
음
                                                                                                                                                   장염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCCAACGCGTGGTCGGAAGGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAT 12-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                     GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 240
                                                                                                                                                                                                                                                                                                    241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
                                     11 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCGGATTCTAATCTTCTAGGTTCTAGGTTCTAGGTTCTAGGTTCTAGGTTCTAGGTTCTAGGTTCTAGGTTCTAGATTTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTCTAGATTAGATTCTAGATTCTAGATTCTAGATTCTAGATTAGATTCTAGATTCTAGATTAGATTCTAGATTAGATTCTAGATTAGATTAGATTCTAGATTAGATTCTAGATTCTAGATTAGATTAGATTAGATTAG
              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGCCCCCCCTCCCATAACTTCCAGCTGTCCCAGGGTGGCCAGGGATTCGCCATTCCGATC
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reed, S.G., Skeiky, Y.A., Campos-Neto, A., Houghton, R.L., Vedvick, T.S., Twardzik, D.R. and Dillon, D.C. Compounds for immuncherapy and diagnosis of tuberculosis Patent: EP 1347055-A 4 24-SEP-2003; CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
99.6%; Score 394.4; DB 6; Length 447;
Best Local Similarity 99.7%; Pred. No. 9e-57;
Matches 395; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 ACAGGGAACGIGACATIGGCCGAGGACCCCCGGCC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA

    .447
    /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447 bp
Sequence 4 from Patent EP1347055.
AX832581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX832581.1 GI:39840631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unidentified
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191
                  ч
                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                           191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 19
AX832581
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
```

g

\$ B \$

පු පු

장염

8 6

8

В

ò

ö

g

Š

ò

Dp

d δ

ਨੇ

g

ठ

g à ą

à

```
DS Unidentified

DS Unidentified

PN JP 20-001-2001

PD 02-007-2001

PP 30-AUG-1996 JP 1997511464

PP 30-AUG-1996 US 08/623436, 22-SEP-1995 US 08/533634 PR

22-MAR-1996 US 08/620874, 05-UUN-1996 US 08/659683 PR

12-UUL-1996 US 08/680574

PI STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS PI RAYMOND HOUGHTON, THOMAS H VEDVICK, DANIEL R TWARDZIK PC C12N15/31, CO7K14/35, A61K38/16, C12N15/6, G01N33/569, C12Q1/68, PC C12N15/10,

PC C12N1/21/A61K39/04, (C12N1/21, C12R1:19)

CC Strandedness: Single;

CC Topology: Linear;

CC Compounds and methods for immunotheraby and diagnosis of CC
                                                                                                                                                                                                                                                                                                                                                                                                      BD069285 447 bp DNA linear PAT 27-AUG-2002 Compounds and methods for immunotherapy and diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGCCAGGCGATGGCGATCGCGGCCAGATCCGATGGGGGGGTCACCCCACCGTTCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 ATCACCGCGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 310
                                                                                                     gogcarcancecogergacercarcresersacerasecaaaceaaagecaaegecaeges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ATCGGGCCTACCGCCTTCCTCGGCTTTGTCGACAACAACGGCAACGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 ACGGCCGCGTCCGATAACTTCCAAGCTCTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                           Reed, S.G., Skelky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.H. and Twardzik, D.R. Compounds and methods for immunotherapy and diagnosis of Patent: JP 2001517069-A 4 02-0CT-2001;
241 ATCACCGCGGCGGCGCGCTCCGATCAACTCGGCCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C12N1/21//A61K39/04, (C12N1/21,C12R1:19)
Strandedness: Single;
Topology: Linear;
Compounds and methods for immunotherapy and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism='Unidentified'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
99.6%; Score 394.4; DB 6;
Best Local Similarity 99.7%; Pred. No. 9e-57;
Matches 395; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                    361 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 396
                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BD065285.1 GI:22614888
JP 2001517069-A/4.
unidentified
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to 447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    표되되
                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                RESULT 22
BD069285
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                    요 요
                                                                                                                                                          셤
                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MICHAEL J LONGONION, INCURS S VENTICAL DANIEL R INARCOLL, FIL

MICHAEL J LONGONION, INCURS S VENTICAL DANIEL R INARCOLL, FIL

MICHAEL J LONG S AGIKAS/04, AGIKAS/06, AGIKAS/06, AGIKAS/06, CI2NIS/31, CO7K14/35, AGIKAS/06, GOIN33/56, CI2NIS/19, CI2NIS/21, PC

CI2NIS/10/, CI2RIS/31, CI2RIS/31, PC

CI2NIS/10/, CI2RIS/31, CI2RIS/31, PC

CC Topology: Linear; Location/Qualifiers

FT Rey

FT Source Location/Qualifiers

FT H Rey

Location/Qualifiers

Location/Qualifiers

Location/August Linear; Location/August Linear; Location/August Linear; Line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arcedectraccectriceredectreserengicalearareacaaceaeceaecea 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GICCAACGCGIGGICGGGAGCGCTCCGGCGAAGICTCGGCATCTCCACCGGCGACGIG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GICCAACGCGIGGICGCGGAGCGCTCCGGCGAGTCTCTCGGCATCTCCGCCGGCGACGTCTC
                                                                                                                                                                                                                                                                                                                                            PAT 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/818112 PI
ANTONIO CAMPOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360
                                                                                    GGGCATCATCCCGGGGACGTCATCTCGGTAACTGGCAAACCAAGTCGGGCGGCGCGCGT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACGGCCGCCGCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unclassified.
1 (bases I to 447)
1 (bases I to 447)
Vedvick, T.S., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.S., Twardzik, D.R. and Lodes, M.J.
Compounds and methods for immunotherapy and diagnosis of Patent: JP 2001501832-A 4 13-FBB-2001;
CORIXA. CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAYMOND HOUGHTON, THOMAS S VEDVICK, DANIEL R TWARDZIK, PI
                                                                                                                                                                                                                                                                                                                                         BD006445 11near PAT bp DNA linear PAT Compounds and methods for immunotherapy and diagnosis of Tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.6%; Score 394.4; DB 6; Length 447; Best Local Similarity 99.7%; Pred. No. 9e-57; Matches 395; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OS Unidentified
PN JP 2001501832-A/4
PD 13-FEB-2001
PF 07-00797 JP 1998518456
PR 11-OCT-1996 US 08/730510,13-MAR-1997 US
STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                      371 AcAddaAcdraAchradccaAddaAccccddad 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .447
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BD006445.1 GI:18634816
JP 2001501832-A/4.
unidentified
unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                3D006445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NETO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191
                                              301
                                                                                                   311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
SOURCE
                                                                                                                                                                                                                                                                                          RESULT 21
BD006445
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
```

ô

à 원 Š g à g à g

130 180

70 9

à d TITLE

SOURCE

ORIGIN

δ g 임

ò

a

ò

d ò QC QC ઠે ద ઠે

ò

```
JOURNAL Patent: US 6350456-A 17 26-FEB-2002;
ATURES Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1872 bp | 1
Sequence 17 from patent US 6458366.
                                             /organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AR233110.1 GI:27275546
                                 .1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown
                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 27
AR233110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                 쉽
                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                     ŝ
                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                 Unclassified.

1 (bases 1 to 1872)
Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for diagnosis of tuberculosis
Patent: US 6338852-A 17 15-JAN-2002;
1 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1058 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGGCACGCGT 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAT 20-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   998 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAAC 1057
                                                                                                                 PAT 20-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCCACCGTTCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           878 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCGCACGA 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          938 GTCCAACGCGTCGGAAGCGCTCCGGCGAAGTCTCGCATCTCCACCGGCGTG 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GGGCATCATCCCGGGTGACGTCATCTCGGGTGACCTGGCAAACCAAAGTCGGGCGCGCACGCGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.

1 (bases 1 to 1872)

Reed,S.G., Skeiky,Y.A.W. and Dillon,D.C.
Compositions and methods for the prevention and treatment of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 1872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                 linear
                      1118 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1118 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.8%; Score 391.2; DB 6 Best Local Similarity 99.2%; Pred. No. 2.4e-56; Matches 393; Conservative 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1872 bp I
Sequence 17 from patent US 6350456.
AR194838
                                                                                                          Sequence 17 from patent US 6338852. AR182455. AR182455.1 GI:20225662
                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
/wol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AR194838.1 GI:20244275
                                                                                                                                                                                                  Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unknown
                                                                                                                                                                                                                    Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 26
AR194838
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                              DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                    ORGANISM
                                                                              RESULT 25
AR182455
LOCUS
                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                      FEATURES
```

```
Unclassified.

Unclassified.

1 (bases 1 to 1872)

Reed(S.G., Skeiky,Y.A.W., Dillon,D.C., Campos-Neto,A., Houghton,R., Nedvick,T.S., Twardzik,D.R., Lodes,M.J. and Hendrickson,R.C.
Compounds and methods for diagnosis of tuberculosis
Patent: US 6458366.A 17 01-OCT-2002;
Patent: US 6458366.A 17 01-OCT-2002;

Location/Qualifiers

1 . 1872

/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1058 GGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGCGCCACGCGT 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear PAT 20-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
                                                                                                                                                                     817
                                                                                                                                                                                                                                                                                 877
                                                                                                                                                                                                                                                                                                                                                                                               937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           938 Greenacecercerceanecerrecescescanererresecarerecescences 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             758 ACGCCCCCCCCATAACTICCAGCTCTCCAGGTGGGCAGGGATTCGCCATTCCGATC 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCGCACGA 180
                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                878 AICGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GICCAACGOGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                 1 ACGCCCCCCCCATAACTTCCAGCTCTCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                     758 AcceccecercechraAcriccacinereccacecicaceacacacacarreccarreccare
                                                                                                                                                                                                                                1 ACGGCCGCCTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 98.9%; Score 391.2; DB 6; Length 1872; Best Local Similarity 99.2%; Pred. No. 2.4e-56; Matches 393; Conservative 0; Mismatches 3; Indels 0;
Query Match 98.8%; Score 391.2; DB 6; Length 1872; Best Local Similarity 99.2%; Pred. No. 2.4e-56; Matches 393; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1118 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

ઠે ద 8 6 ò g δ 유 ઠે

g

us-09-684-215b-3.rge

```
1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 12-DEC-2003
                                                                                                                                                                           Reed, S.G., Skeiky, Y.A., Dillon, D.C., Campos-Neto, A., Houghton, R.L., Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for immunotherapy and diagnosis of tuberculosis of tuberculosis of tuberculosis.

Patent: EP 1203817-A 17 08-MAY-2002;
CORIXA CORPORATION (US)

Location/Qualifiers
                                                             PAT 21-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360
                                                                                                                                                                                                                                                                                                                                                                                                                               817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCGCACGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               758 ACGGCGCGCTCCAAACTTCCAGCTGTCCCAAGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
Reed, S.G., Skeiky, Y.A., Campos-Neto, A., Houghton, R.L.,
Vedvick, T.S., Twardzik, D.R. and Dillon, D.C.
                                                                                                                                                                                                                                                                                                                                                      6; Length 1872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                  98.8%; Score 391.2; DB 6; Length ilarity 99.2%; Pred. No. 2.4e-56; Conservative 0; Mismatches 3; Indels
                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1118 ACAGGAACGTGACATTGGCCGAGGACCCCCGGCC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCCGGCC 396
1118 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 1153
                                                                                                                                                                                                                                                                         1. .1872
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX832594 1 from Patent EP1347055. AX832594.1 GI:39840644
                                                              1872 bp
Sequence 17 from Patent EP1203817.
                                                                                         AX429609
AX429609.1 GI:21540858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unidentified
unidentified
unclassified.
                                                                                                                             unidentified
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 393; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            878
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 30
AX832594
LOCUS
DEFINITION
                                                                          DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                        RESULT 29
AX429609
LOCUS
                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             상 . 원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \dot{\delta}
  셤
                                                                                                                                                                                                                                                                                                                                                                               Unclassified.

Unclassified.

Unclassified.

Unclassified.

Unclassified.

Unclassified.

Unclassified.

S Red, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C.

Compounds and methods for immunotherapy and diagnosis of tuberculosis

Compounds and methods for immunotherapy and diagnosis of tuberculosis

Location/Qualifiers

Location/Qualifiers

1. 1872

Arch_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 ATCACCGCGGTCGACGCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
                                                                                                                                                                          ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGACGACGGCGCACGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 17-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Greenhedecardareagangegreegecagechharreagantereagangang 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360
                                                      240
                                                                              997
                                                                                                        241 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
    180
                  878 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCACACGGCGCACGA 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                     938 GTCCAACGCGTGGTCGGCAAGCGCTCCGGCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                           301 gagcarcarcarcarcarcarcarcarcarcarcaraaccaaarcaaarcaaaraacaa
                                                       GTCCAACGCGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 1872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 98.8%; Score 391.2; DB 6; Length 1 sl Similarity 99.2%; Pred. No. 2.4e-56; 393; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                              361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                        AR353315
Sequence 17 from patent US 6592877.
AR353315.
AR353315.1 GI:33759121
                                                                                                                                                                                                                                                                                                                                                                          Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S:
Matches 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              938
        121
                                                         181
                                                                                                                                                                                                                                                                               RESULT 28
AR353315
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
```

g

8 8

8 8 8

셤 à 요 상

ö

```
998 ATCACCGGGGTCGACGGCTCCGATCAACTCGGCCACGCGATGGCGGAAGGCGCGTTAAC 1057
                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                       121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GGGCATCATCCCGGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGCGT 360
                                                                                                                                                                                                                                                 61 GGGCAGGCGATGGCGATCGCGAGGCCAGATCGGGTGGGGGGTCACCCCACCGTTCAT 120
                                                                                                                                                                                                                                                                                                                                                                          181 GICCAACGCGIGGICGGAGCGCICCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 240
                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                            1 ACGCCCCCGTCCCGATACTTCCAGCTCTCCCAGCTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                             0; Gaps
Compounds for immunotherapy and diagnosis of tuberculosis Patent: EP 1347055-A 17 24-SEP-2003; CORIXA CORPORATION (US)
Location (Us)
1. .1872
/ organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
                                                                                                                                                               Query Match

98.8%; Score 391.2; DB 6; Length 1872;
Best Local Similarity 99.2%; Pred. No. 2.4e-56;
Matches 393; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1118 ACAGGGAACGTGACATTGGCCGAGGAACCCCCGGGCC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                       source
     TITLE
JOURNAL
                                                      FEATURES
                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                            à
```

Search completed: April 30, 2004, 07:06:10 Job time : 6636 secs

49.2 12.4 561 28 BH020987 48.6 12.3 634 10 BE361689 47.8 12.1 831 28 CC334434 47.6 12.0 289 29 P8641 47.4 12.0 731 13 BX626840	47.4 12.0 935 29 CNSO06XK 47 11.9 1009 29 CNSO10EW	12 46.4 11.7 515 13 BX424977 13 45.8 11.6 472 14 CB620050 14 45.6 11.5 515 13 BX424977 15 45.4 11.5 446 29 CC992789	16 45.4 11.5 459 28 CC349367 17 45.4 11.5 582 29 CG244774 18 45.4 11.5 707 29 CCG78226 19 45.4 11.5 777 29 CG386745	20 45.4 11.5 802 29 CG326739 21 45.4 11.5 830 28 CCG31586 22 45 11.5 1148 14 CK161968	44.8 11.3 502 9 AU191977	44.6 11.3 839 29 CNS004NB 44.6 11.3 1200 13 BX456467	44.6 11.3 1201 13 BX360624 44.4 11.2 496 12 BJ307565 44.4 11.2 504 28 BHJ30076	30 44.4 11.2 590 28 BH189840 31 44.4 11.2 632 28 BH189865 32 44.4 11.2 932 29 CNSO072Q 33 44.2 11.2 844 29 CNSO052P	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	44 11.1 729 14 CF482692 ALIGNMENTS	RESULT 1 U82114 LOCUS U82114 DEFINITION U82114 occered cosmid library Mycobacterium leprae genomic clone cosmid L-373; contig 64, genomic survey sequence.		_		MEDLINE 99003183 PUBMED 9784577 COMMENT Contact: Silbag FS Microbiology Colorado State University	Fort Collins, CO 80523, USA Eiglmeier, K., Honore, M., Woods, S.A., Caudron, B. and Cole, S.T. Use of an ordered cosmid library to deduce the genomic organization of Mycobacterium leprae. Mol. Microbiol. 7 (2), 197-206 (1993)
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: April 30, 2004, 04:41:08; Search time 2046 Seconds (without alignments) 5779.777 Million cell updates/sec	Title: US-09-684-215B-3 Perfect score: 396 Sequence: 1 acggccgcgtccgataactttggccgagggacccccggcc 396	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 27513289 seqs, 14931090276 residues	Total number of hits satisfying chosen parameters: 55026578	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database: EST:* 1: em_estba:* 2: em_esthum:* 3: em_estin:* 4: em_estrov:* 5: em_estrov:* 6: em_estrov:* 7: em_estror:* 8: em_htc:* 9: gb_est2:* 10: gb_est2:*	11: gb_htc:* 12: gb_es:3:* 13: gb_es:4:* 14: gb_es:5:* 15: em_estfun:*	16: em_estom:* 17: em_gss_hum:* 18: em_gss_huv:* 19: em_gss_pln:* 20: em_gss_vr:*	22: em_gss_mam:* 23: em_gss_mus:* 24: em_gss_pro:*	25: em_gss_rod:* 26: em_gss_phg:* 27: em_gss_vrl:* 28: gb_gssl:*	מביב.	* Result Query No. Score Match Length DB ID	.2 16.5 289 29 U82114 U

a ઠે ద ò 셤 ਨੇ g

```
Direct Submission

Submitted (02-UIM-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Droscophila Genome Project (BDGP). The BDGP is constructing a physical map of the Droscophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Droscophila melanogaster BAC library was prepared by Kazutcyo Geogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Droscophila DNA provided by the BDGP from the Engle and EST library is named RPCI-98 and was constructed by partial EcoRI digestion of Droscophila DNA provided by the BDGP from the BDGP's pl and EST library is named RPCI-98 and was constructed by partial sogenic strain v2; on bw sp, the same strain used for the BDGP's pl and EST library is named RPCI-98. The same strain and how to order individual BAC clones, the entire library, or filters for hybridization from the BACFAC Resource Center can be located the page of the found at http://bacpac.med.buffalo.edu/droscophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS0091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 TICCGAICGGGCAGGCGAIGGCGAICGCGGGCCAGAICCGAICGGGIGGGGGGGTCACCCA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                           482
                                                                                                                                                                                                                                                                                                                                                                                                                                  260 CTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCCGGTGACG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483 AATCCGTCAAGGACGCCCGCGAGCTCGCCCCACCATCGGCGCGCCCCCCCTCGTGCGA 542
                                                                                  140 TCGGCTTGGGTGTTGTCGACAACAACGGCGCACGACGACGTCCAACGCGTGGTCGGGA 199
                                                                                                                                                                     363 rescentas de contra de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 GCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTCGACGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
94; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.7%; Score 50.4; DB 29;
llarity 15.4%; Pred. No. 4.8;
Conservative 158; Mismatches 133;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila me/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 TCATCTCGGTGACCTGGCAAACCAAG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 rcgranacrrancerccracana 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLY), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="BACR19D16"
clone lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL053013.1 GI:4934461
GSS.
         Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 53; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
CNS0091P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                      쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                8 6
                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA linear GSS 24-APR-2001
library Bradyrhizobium japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobiaceae; Bradyrhizobium.
1 (bases 1 to 603)
1 (bases 1 to 603)
1 (bases 1 to 603)
2 (Bradyrhis, J. P., Wood, T. C., Stacey, M. G., Loh, J. T., Judd, A.,
Golicoebhea, J. E., Stacey, G., Sadowsky, M. J. and Wing, R. A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 CGACAACAACAGGCAAACAGGCGCAACGAGTCCAACGCGTGGGTCGGGAGCGCTCCGGCGAAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACCGCGATGGCGGACGCGTTAACGGCCATCATCCCGGTGACGTCATCTCGGGTGACCTG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 caacecerrocorrecerecearceaacecececeácearcaaacearererera 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ceacaacccceeecccaaacrraresaccreeecceerecreecceere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recciocarreccia a de de contrator de contrato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 TCAGGATCAGTAGCAGTCGCACGGTTCAGGTCACGCCACCGCAAGG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAAACCAAGTCGGGCGCGCACGCGTACAGGGAACGTGACATTGGCCCGAGG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:375"
/lab_host="Rs_coli"
/clone lib="B. japonicum BAC library"
/note="Vector: pIndigo536, Site_1: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                       16.5%; Score 65.2; DB 29; Length llarity 55.2%; Pred. No. 0.0046; Conservative 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bradyrhizobium japonicum"
/mol_type="genomic DNA"
/srain="USDA110"
/db_xref="taxon:375"
                                                                                                                                     /organism="Mycobacterium leprae"
/mol_type="genomic DNA"
_b_xref="taxon:1769"
/clone="cosmid L-373; contig 64"
/clone_lib="ordered cosmid library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55.6; DB 28;
Pred. No. 0.42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Uordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 11 (8), 1434-1440 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BJ Ba0002108r B. japonicum BAC 1
genomic, genomic survey sequence.
AZ934428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 553.
Location/Qualifiers
                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: rwing@clemson.edu
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ934428.1 GI:13776488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.0%;
54.4%;
                      Class: unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21376150
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simil
Matches 127; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
AZ934428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                             ORIGIN
```

661

d

ठे 셤

g

ò

g à

ò

```
BH020987
P864c.d_LEISHPAC-left.1 Leishmania major Friedlin Cosmid Genomic
Library Leishmania major genomic clone P864c, genomic survey
                           340 BCCMCSSSSCCGSASARGVKVRASGGAGKRQGGGGGASASHSSSAACBSSSSSCSASCW 781
                                                                                                                 GATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAA 299
  120 TATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCCAACGGCGCACG 179
                                                                                                                                                                                                                                                                                                   /note="Vector: cLHYG; Site_1: BamHI; Genomic DNA from Leishmania major Friedlin was partially digasted with Sau3AI, size selected, and ligated with BamHI-digested cLHYG cosmid vector DNA. 9216 clones were picked and arrayed. Library construction is described in Ivans et al., Genomics Research, 8:155-145 (1998). The cLHYG vector (Acc. No. CVUS2231) is described in Ryan et al, Gene, 131:145-150 (1993)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mack, J.,
                                                                                                                                                                                                             180 AGTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGT
                                                                                                                                                                                                                                                                          CGGGCATCATCCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Leishmania major Friedlin Cosmid Genomic Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leishmania.

1 (bases 1 to 561)

Myler,P.J., Vogt,C., Cawthra,J., Klacking,M., Marty,A., Mac
Munden,H., Nguyen,D., Robertson,L., Sisk,E., Fazelinia,G.,
Aggarwal,G., Nelson,S., Seyler,A., Worthey,E. and Stuart,K.
Leishmania major Friedlin Cosmid End Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leishmania major
Leishmania major
Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Other GSSs: P864c.d_LEISHPAC-right.1
Contact: Myler PJ Research Institute
Seattle Biomedical Research Institute
4 Nickerson Street, Seatttle, WA 98109-1651, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49.2; DB 28;
Pred. No. 7.5;
0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                       360 TACAGGGAACGTGACATTGGCCGGGGACCCCCGGC 395
                                                                                                                                                                                                                                                                                                                                                                                                 major"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'lab host="E. coli ED8767"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .561
/organism="Leishmania m.
/mol_type="genomic DNA"
/strain="Friedlin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:5664"
clone="P864c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mylerpj@sbri.org
Seq primer: LEISHPAC-left
Class: PAC end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH020987.1 GI:14202102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.6%;
Matches 75; Conservative (
                                                                                                                                                                                                                                                                               300
                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
BH020987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRIGIN
                                                                                      à
                                                                                                                              ద
                                                                                                                                                                   ð
                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                             g
                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission

Submitted (02-UN-1999) Genoscope - Centre National de Sequencage:
Submitted (02-UN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqrefégenoscope.cns.fr - Web: www.genoscope.cns.fr - Web: www.genoscope.cns.fr - Genermination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs: For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RECI-99 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pland by to corder individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL053013
GI:4934461
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
613 TSBSCSCCCSSKSVCGTSCSSSSSSCSSSSSTSKSSSSSSSSSSSSSSSTTS 672
                                                                                                GCGCACGAGTCCAACGCG-TGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACC 231
                                                                                                                                                              GGCGACGTGATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGAC 291
                                                                                                                                                                                                                                                         GCGCTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGC 351
                                                                                                                                                                                                                                                                                                      793 GISSSSDSISICCSCCCCYMCICCSIYBMBCYISISCGGSSSSSGKGGVTKCGCGGCGSSS 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNSSBCSSCSSSBSSSTSSMSSSSBSSSSSSSSSSGTSSACVKCNASSSCGCCGCGMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebydroidea; Drosophildae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 925;
                                                                                                                                                                                                                                                                                                                                                                             GGCACGCGTACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 157; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.5%; Score 49.6;
12.8%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   006
                                                                     173
                                                                                                                 673
                                                                                                                                                              232
                                                                                                                                                                                                                                                         292
                                                                                                                                                                                                                                                                                                                                                     352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
CNS0091P/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
```

ö

à

```
P864L 1inear GSS 25-JUL-2000 Leishmania major Friedlin PAC P864 left end-sequence, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC334434 6SS 16-MAY-2003 OGAGAG83TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0365N21, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 TCTCCACCGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 TGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      662 GCGCTTCCGGTCCGGCGGCCCTCCTCCGCGACGTCCTCTCCTCCTCCTCGCGTCG 603
257 GCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCCGGTG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                              1 (bases 1 to 831)
Whitelaw(C.H., Quackenbush, T., Van Aken, S., Utterback, T.,
Rhistor, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   722 redecade erecidade recede de consecue 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 ACGGCAACGGCGCACGAGTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain=BR3"
/strain=BR3"
/clone="ZMMBMa0365N21"
/clone="ZMMBMa0365N21"
/clone="Wector: pBCSK-; Site 1: Hincl!; 0.7-1.5
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.1%; Score 47.8; DB 28; Length 831; larity 57.1%; Pred. No. 15; Conservative 0; Mismatches 77; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seg primer: Tel:
Class: sheared ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                           88 Gérecercércérececene 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Cathy Whitelaw
TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC334434.1 GI:30803847
GSS.
                                                                                                                                                                                                                                                  317 ACGTCATCTCGGTGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 AGTCGGGCGGC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602 ccccccccccccc 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 109; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P864L
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
CC334434/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                    셤
                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sorghum bicolor (sorghum)
Sorghum bicolor
Sorghum bicolor
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
El (bases I to 634)
Sordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and
Pratt, L.H.
An EST database from Sorghum: dark-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Contact: Gordonnier-Pratt MM
Contact: Gordonnier-Pratt MM
Contact: Gordonnies and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA linear EST 20-JUL-2000 (DG1) Sorghum bicolor cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sorghum bicolor"
/mol type="mRNA"
/db Xref="taxon:4558"
/clone lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
lambda Zap; Site_1: XhoI; Site_2: EoCRI; The library was
made from poly-A RNA in the cloning vector lambda ZaP II.
Clones to be sequenced were prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 Aceacerecedrocaderaerecadadecerrieresececicadececresecerisécia 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 recedence de antice de recedence de contrara recedencia de contrara de cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 ICCTCGGCTTGGGGTGTTGTCGACAACAGCAACGGCGCACGAGGTCCAACGCGTGGTCG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ececcéccecececes de la contract de l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTCGACG 256
      159 CAACAACGGCAAACGGCGCACCAAGTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76
                                                                                                    13 CGAGATCGGCATCGCCGGCCGGCTGGTAGTCGAGGGCGCGTCGGGTCCCGCGGCTCGCGT 72
                                                                                                                                                                                                                                                        276
                                                                                                                                                                                                                                                                                                                                                                           130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 ACTICCAGCIGICCCAGGGIGGGCAGGGAITCGCCAITCCGAICGGGCAGGCGAIGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 Acceptrices en anterior de la constante de la contra del contra de la contra del l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                         ceecarctaccacceaceaecarcacceceeceaceaeceecearcaactceecc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.3%; Score 48.6; DB 10; Length 634; Similarity 47.0%; Pred. No. 10; Conservative 0; Mismatches 169; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE361689 634 bp
DG1 81_E06.91_A002 Dark Grown 1
sequence.
BE361689 GI:9303246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: PolyTMix
High quality sequence start: 67
High quality sequence stop: 634
PoLYANO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Simil
Matches 150; C
                                                                                                                                                                                                                                                        219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
BE361689/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                    g
                    ò
                                                                                                                         g
                                                                                                                                                                                                                                                        ò
```

ä

663

```
/organism="Anopheles gambiae"
/mol_type="mRNA"
/db_xref="taxon:7165"
/clone="ANGNP1222C12T7"
                                                                                                                                                                                                                                                                                                                                            Query Match 12.0%;
Best Local Similarity 51.2%;
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
CNSO06XK
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
           FEATURES
                                                                                                                                                                                                                                                                                                              DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                         Submitted (24-JUL-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 18A, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk and see http://www.eb1.ac.uk/parasites/leish.html
Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L_major/
The primer sequence can be obtained from alicat@sanger.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX626840
BX626840 NAP1 Anopheles gambiae cDNA clone ANGNP1222C12T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 CAACAACGGCAACGGCGCACGAGTCCAACGCGTGGGTCGGGAGCGCTCCGGCGGCAAGTCT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 CGGCATCTCCACCGCGCACGTGATCACCGCGGTCGACGCGCTCCGATCAACTCGGCC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T. (bases 1 to 731)
Lobo,N.L., Gardner,M., Romans,P. and Collins,F.H.
Anopheles gambiae EST, Center for Tropical Disease Research and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 cakakacidecknicecidecedecriernikaridaddecercedenicededdecerceden
                                                                                                                                                  Ivens, A.C., Lewis, S.M., Bagherzadeh, A., Zhang, L., Chan, H.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
                                                                                                                                                                                                                                                                2 (bases 1 to 289)
Taylor, R.G., Huckle, E.B.J., Ivens, A.C., Rajandream, M.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                               Sukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.0%; Score 47.6; DB 29; Length 289; larity 62.7%; Pred. No. 13; Conservative 0; Mismatches 44; Indels 0
                                                                                                                                                                                  Smild.n.v.r.
A physical map of the Leishmania major Friedlin genome
Genome Res. 8 (2), 135-145 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2003)
Contect: Frank H. Collins
Contect: Frank H. Collins
Center for Tropical Disease Research and Training
University of Notre Dame
Notre Dame, IN 46556, USA
Tel: 574-631-3945
Fax: 574-631-3996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Leishmania maj'
mol_type="genomic DNA"
| Strain="Friedlin"
| db xref="taxon:5664"
| clone="PAC P864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX626840.1 GI:33553685
                 AL390548
AL390548.1 GI:9501524
                                                                                                                                     (bases 1 to 289)
                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                    Leishmania major
Leishmania major
survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                       Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       raining
                                                                                                                                                                                                                                98146435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Simil
Matches 74; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                      SOURCE
                                                                                                                                                                                        TITLE
JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
BX626840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                   ACCESSION
                                                                                                                                                         AUTHORS
                                  VERSION
KEYWORDS
                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
```

```
/lab host="E. coli DH10B"
/clone into-"Napl"
/clone itb="Napl"
Site 2: EcoRI; ESTS sequenced from the T7 priming site
that reads from the 5' end of cDNA. The Napl is a
directionally cloned and normalized, oligory primed cDNA
library constructed from a mixture of Anopheles gambiae
developmental stages according to: Bonaldo, Lennon &
Soares (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery, Genome Research
6, 791-806."
frank.h.collins.75@nd.edu.
Location/Qualifiers
    Email:
```

ö 156 CGACAACAACGGCAACGGCGCACGAGCTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAG 215 49 caacaacaacaacaacaacaacaacaacaacaacacacaacaacaaacaaaca 108 276 CACCGCGATGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTG 335 216 TCTCGGCATCTCCACCGGCGACGTGATCACCGGGGTCGACGGCGCTCCGATCAACTCGGC 275 169 chocegrafiedodecodocedacegroedocarcacacedecareacegedegeaaarcac 228 ö Score 47.4; DB 13; Length 731; Pred. No. 18; 0; Mismatches 106; Indels 0; 336 GCAAACCAAGTCGGGCGCGCACGCGTACAGGGAACGTG 372 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ALO66051.
ALO66051.1 G1:4945019 Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

Direct Submission

Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage :
Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGe. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Prosophila DNA provided by the BDGP from the isogenic strain v2: cn bw sp, the same strain used for the BDGP's pland and EST libraries. A more detailed description of the library

```
mRNA linear EST 15-MAY-2003
Homo sapiens cDNA clone CL0BA005ZH04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 CTCGGCATCTCCACCGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 515)
1 (hase, Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY Cedax - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6304.f For
more information about this ,cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CLOBAOSZHO4FPL&cluster=6304.f. Contact
Feng Liang Email: fliangalifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBA005ZHO4FP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           882 RSWGCGCGGSGSSGGGGCSCSCCCCNCGRCGGCGGCGACGCSSGSSCGSSGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCAGGGATTCGCCATTCCGATCGGGCGATGGCGATCGCGGCCAGATCCGATCG
                                                                                                                                                                                                                                                                                                                                                             277 ACCGCGAIGGCGGACGCGCTTAACGGGCAICAICCCGGIGACGTCAICTCGGIGACCIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 CAAACCAAGTCGGGCGCCACGCGTACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGGGGGGTCACCGTTCATATCGGGCCTACGGCCTTCCTCGGCTTGGGTGTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                              942 GGCGMSGSAGCRCSCCGGGGGGGSCSCCSCCSSCCSCCSSSGGGCSSSGNGMSGSKGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 GACAACAACGGCAACGGCGCACGAGTCCAACGCGTCGGGAGCGCTCCGGCGGCAAGT
                                                                                                                                                                                                                                                 Length 1009;
                                                                                                                                                                                                                                              11.9%; Score 47; DB 29; Length 10
.larity 30.8%; Pred. No. 23;
Conservative 80; Mismatches 168; Indels

    1009
    organism="Drosophila melanogaster"

                                                                            /mol type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACNO3P19"
/clone lib="brosBAC"
/plasmid="pBeloBACI1"
/note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX424977
BX424977 Homo sapiens PLACENTA H
3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX424977.1 GI:30784421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                       Local Similarity
Les 111; Conserv
pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
                                                                                                                                                                                                                                                                                                                                    37
                                                                                                                                                                                                                                                                                                                                                                                                                          97
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
BX424977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                        FEATURES
                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1009 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN03P19 of DrosBAC library from Drosophila melanogaster (fruit AL098882 AL098882.1 GI:5610493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ಹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submission
Submission
BP 191 91006 EVRY Gedex - FRANCE (B-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre droid et Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheron and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 CATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGTACA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGAGTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACGCGTGGTCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 ACCGCGGTCGACGCCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGG 303
                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BBSYSTCSCTBCTKCSSGCSTGSGCTGCCGGGSGCGGCGGGGGGGGGGGGSSS
                                                                                                                                                                                                                                                                                                                                                                                        GCSTCCMYMSSSVSCCSCSGTCCGYCSSCTSCNCSCTYGCKCGCGCGCSTSCSSSCCS
                                                                                                                                                                                                                                                                                                                                                             4 GCCGCGTCCGATAACTTCCAAGCTGTCCCAAGGGTGGGCAAGGGATTCGCCATTCCGATCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
  and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                DB 29; Length 935;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                       /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db xref="texcn:7227"
/clone="BACR14N09"
/clone lib="RRCI-98"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                       89; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 GGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dsgssggcgsgagascsgagasccscscacac 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                    19
                                                                                                                                                                                                                                                                              12.0%; Score 47.4; 28.2%; Pred. No. 19
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    703
                                                                                                                                                                                                                                                                                                                                                                                                                 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
CNS010EW/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                            FEATURES
```

g

ð

d à d à d à d ò

셤 ò 336

704

644

763

883

96

Gaps

۲,

ö

Gaps . 0 221

86

206

g ð g ò

8 ద ò

```
/organism="Homo sapiens"
//organism="Homo sapiens"
//db itype="mRNA"
//db xref="text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="Text-organism="T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Genoscope
Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
BP 191 9106 EVRX cedex - France
BRail: seqref@qenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6304.f For
more information about this cluster, see
more information about this cluster, see
cgi-bin/cluster.cgi?seq=CLOBA005ZH04FPL&cluster=6304.f. Contact:
Feng Liang Enail: fliang@lifetech.com URL
Feng Liang Enail: fliang@lifetech.com URL
Faraday Avenue Genoscope sequence ID: CLOBA005ZH04FPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  515 bp mRNA linear EST 15-MAY-2003
BX424977 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA005ZH04
BX424977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 GOCGOCAAGICTCGGCATCTCCACCGGCGACGTGATCACCGCGGGGGGCGCTCCGAT 266
                                                                                   +; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 GAICCGAICGGGIGGGGGICACCCACCGTICAIAICGGGCCIACCGCCTICCICGGCTI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 daaggcgaaggcgacgacgaggcactccactgctrcccaagcrggcgrgcccgaggg 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 creitracide de carcardada de constructados de contracides de contraciones de contracio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 decendedarchaccertradadecedecidedecidededecertrancadedecedec 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens

Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Buteleostomi;

Mammalia; Butheria, Primates; Catarrhini; Hominidae, Homo.

1 (bases 1 to 515)

1 (bases 1 to 515)

Pull-length cDNA libraries and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 GTCCCAGGGTGGGCAGGGATTCGCCATTCCGATCGGGCAGGCGATGGCGATCGCGGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 GGGTGTTGTCGACAACAACGGCGCGCACGAGTCCAACGCGTGGTCGGGAGCGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 CAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCCGGT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 472;
                                                                                                                                                                                                                                                              Score 45.8; DB 14; Length
Pred. No. 34;
0; Mismatches 152; Indels
/lab_host="DH10B"
/clone_lib="OSITBs"
/note="Vector: pBluescript II KS
Xhol; Lesion Mimic SPL 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX424977.1 GI:30784421
                                                                                                                                                                                                                                                                        11.6%;
ilarity 47.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                         al Similarity
137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST
                                                                                                                                                                                                                                                                             Query Match
Best Local Si
Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
BX424977/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contract sativa (indica cultivar-group)

Cyza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatcophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatcophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Brhartoideae; Oryzeae; Soderlund, C., Wing, R. and Wang, G. Large-scale identification of ESTs involved in the interaction of Unpublished (2003)

Contact: Rod Wing

Lizona Genomics Institute
University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

BST21-0088, USA.
                                                     /clone="CLOBA005ZH04"
/tissue type="PLACENTR"
/clone_lb="Homo sapiens PLACENTR"
/note="Vector: PCMVSPORT 6; 1st strand cDNA was primed
/note="Vector: PCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and SCRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CB620050 472 bp mRNA linear BST 08-APR-2003 OSIIEB04P23.f OSIIEA Oryza sativa (indica cultivar-group) cDNA clone OSIIEA04P23 5', mRNA sequence.
CB620050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 TTGGGGSSSSSSSSSSAAARAAVSVVSSSGGGGGCSSSSSSVSSSSSSSSSS 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGGGTGTTGTCGACAACAACGGCAACGCGCACGAGTCCAACGCGTGGTCGGGAGCGCT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 CCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGGGGGTCGACGGCGCTCCG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 ATCAACTCGGCCACCGCGATGGCGGACGCGTTAACGGGCATCATCCCGGTGACGTCATC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa (indica cultivar-group)"
/mol type="mRNA"
/cultivar="IR36"
/db xref="taxon:39946"
/clone="GosIEao4P23"
/tisuuc type="Laaf"
/dev_stage="3 week"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.7%; Score 46.4; DB 13; Length Best Local Similarity 10.4%; Pred. No. 26; Matches 23; Conservative 115; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 TCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGTACAGGG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 04 row: P column: 23
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: http://genome.arizona.edu
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB620050.1 GI:29615037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CB620050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
```

us-09-684-215b-3.rst

ω

유

g ò g

 $\dot{\delta}$ g

ò

```
CG234774 S82 bp DNA linear GSS 22-AUG-2003 OG2BL96TV ZM 0.7 1.5 KB Zea mays genomic clone ZNWBMa0753024, genomic survey sequence.
CG334774 GC334774.1 GI:34134660
GSS-4774.1 GI:34134660
                                                                                                                                                                                                                    459 bp DNA linear GSS 16-MAY-2003 OGTABT3TV ZM 0.7_1.5_KB Zea mays genomic clone ZMMBMa0387M02, genomic survey sequence. CC349367 CC349367.1 GI:30818774 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 ACGGCAACGGCACGAGTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 TCTCCAACCGGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bukaryota, Viridiplantae, Streptophyta, Eukaryota, Magnoliophyta; Liliopsida, Poales, Poaceae, PACCAD Clade, Panicoideae, Andropogoneae, Zea.

(Dases 1 to 459)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunberg, A., Rabbins, D. and Lakey, N. Rohlfing, T., Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 gederrnecagneagacadagacerecreagadarenereretereereteragae 273
284 TEGCEGACECETTAACEGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446 Acedecacedes de caraces de control de co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 TGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACC
                                                 191 GCGCCTTCCGGTCCGGGGGCGCCTCCTCCGCGAAGTCCTCTCCTCCTCCTCCTCGCCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4577"
/clone="zwmBM&0397M02"
/clone="b=zm_0.71.5_KB"
/note="Vector: pBCEx-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Fax: 301-838-0208
Famil: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
11.5%; Score 45.4; D
Best Local Similarity 57.5%; Pred. No. 40;
Matches 103; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. 459
7. organism="Zea mays"
//mol_type="genomic DNA"
/gtrain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2002)
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
DEFINITION
                                                                                                                                                                                                               RESULT 16
CC349367/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 17
CG234774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                  ઠે
                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM Zea mays

Subaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Subaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicodeae; Andropogoneae; Zea.

1 (bases 1 to 446)

S Whitelaw, C.A., Quackenbush, J., Van Aken S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citck, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

L Unpublished (2002)
Other GSSs: ZUREQ44TV

Contact: Cathy Whitelaw

TIGR
Fax: 301-838-5843
Fax: 301-838-5843
Fax: 301-838-5843
Fax: 301-838-5843
Fax: 301-838-6848
Cattion/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 bp DNA linear GSS 18-AUG-2003
Genomic survey sequence.
CC992789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4577"
/clone="xwBPa0044H15"
/clone=lib="zm3.0_4.0_KB"
/note="Vector: pBCSK-; Site_1: HincII; 3-4 kb 'unfiltered'
genomic DNA library"
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 ACGGCAACGGCGCACGAGTCCAACGCGTGGTCGGGGGCGCTCCGGCGGCGAAGTCTCGGCA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 TOTOCACOGGOGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 Acedecacedededas Acedececerros respectos de Acedecaces de Company de Acedecacedos de Acedecacaces de Acede
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 CCGATCGGGTGGGGGGTCACCCACCGTTCATATCGGGCCTACCGCCTTCCTCGGCTTGGG 149
                                                                                                                                                                                                                                 150 TGTTGTCGACAACAACGGCAACGGCGACGAGGTCCAACGCGTGGTCGGGAGCGCTCCGGC 209
                                                                                                                                                                                                                                                                                                                                                                                                210 GGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Gaps
                                                                                                   Gaps
                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
11.5%; Score 45.4; DB 29; Length 446;
Best Local Similarity 57.5%; Pred. No. 40;
Matches 103; Conservative 0; Mismatches 71; Indels 5
                  DB 13; Length 515;
                                                                                          71; Indels
         Query Match
11.5%; Score 45.6; Di
Best Local Similarity 8.6%; Pred. No. 37;
Matches 17; Conservative 110; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 CICGGCCACCGCGAIGGC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSSSGCCCCCSSSBBSBB 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC992789.1 GI:33852665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
CC992789/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
```

ij

Gaps

342

d ò

ઠે d us-09-684-215b-3.rst

a

Page

ä

Gaps

중

65

184

TIGR

FEATURES

ORIGIN

ВÞ

g ð

à

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

```
CG326745 11.5 KB Zea mays genomic clone ZMMBMa0742F14, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lose mayo

Lukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Calde; Panitocideae; Andropogoneae; Zea.

1 (bases 1 to 77)

Whitelaw, C.A., Guackenbush, J., Van Aken, S., Utterback, T.,

Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Other GSSs: OGCAH31TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 TGGCGGACGCGTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 Acelegcacecececas Asececraceres de la Acelega de la Ace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 TCTCCACCGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 ACGGCAACGGCGCACGAGTCCAACGCGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 GCGCTTCCGGTCCGGCGGGCGCTCCTCCGCGACGTCCTCCTCCTCCTCCTCGCCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xrefe"taxon:4577"
/clone="zxwBMA0742F1"
/clone=lb="zw 0.7_1.5_KB"
/clone=lb="zw 0.7_1.5_KB"
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                             1. 7017

| organism="Zea mays" |
| /organism="Zea mays" |
| /mol_type="genomic DNA" |
| strain=ng73" |
| /db_xref="taxon:4577" |
| /clone="ZMMBMa0561P03" |
| /clone="Yector: pBCSK-; Site 1: HincII; 0.7-1.5 |
| methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.5%; Pred. No. 44;
Matches 103; Conservative 0; Mismatches 71; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Fax: 301-84-1940 Fax. Seg primer: TP Seg primer: TP Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
11.5%; Score 45.4; DB 29;
Best Local Similarity 57.5%; Pred. No. 45;
Matches 103; Conservative 0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
     Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG326745
CG326745.1 GI:34244011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 19
CG326745/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
DEFINITION
                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OGWESSETV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0561P03, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Busarycta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 70)

Whitelaw, C.A., Ouackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedall, J.A., Rohlfing, T., Clerk, R.W., Numberg, A., Robbins, D. and Lakey, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 ACGGCAACGGCGCACGAGTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 Acesecacececaces and a descention de la constanción de la constante de la 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 TCTCCACCGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 582)

Whitelaw, C.A., Ouackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Unpublished Consortium for Maze Genomics
Unpublished OG2BL96TH
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 TGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Zea mays"
/mol_type="genomic DNA"
/strain="Barner"
/db xref="taxon:4577"
/clone="XMWBNa0753024"
/clone="XMVor71.5_KB"
/note="Voctor: pBGGK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 11.5%; Score 45.4; DB 29; Length 582; Best Local Similarity 57.5%; Pred. No. 42; Matches 103; Conservative 0; Mismatches 71; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301-838-5843
Fax: 301-838-0208
Bmail: whitelaw@tigr.org
Seg primer: TF
Class: sheared ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC678226.1 GI:32083002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1, .582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGE
```

VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

DEFINITION

ACCESSION

RESULT 18 CC678226

ä

Gaps

```
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
DEFINITION
                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 22
CK161968
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG326739 802 bp DNA linear GSS 26-AUG-2003
CG2AH31TH ZM 0.7 1.5 KB Zea mays genomic clone ZNMBMa0742F14,
genomic survēy sēquence.
CG326739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Wagnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 802)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Baddman, M.A., Bedall, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Other GSS: OGZARJITU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 ACGCCAACGCCCACGAGTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442 Acesecacedeses de a reconstrución de la contración de 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 TCTCCACCGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497 rececialectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalectrocalec
164 ACGGCAACGCCACGACGACCCAACGCGTCGGGAGCGCTCCCGGCGCAAGTCTCGGCA 223
                                                                                                                                                                                                                                                                  TCTCCACCGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGA 283
                                                                                                                                                                                                                                                                                                                                                                                        664 rosconocacos de receses de constantes de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 TGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCTCGCTGACCTGGCAAACC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                719 AcGGGACGCGCAGAAAGGCCGCTTCGTCGTCCGGCAGCATCGGCGG-----CTGCCCG 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 TGGCGGACGCGTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/mol_type="genomic DNA"
/grain="BA3"
/db xxef="txen:4577"
/clone="ZMMBMa0742F14"
/clone llb="ZM 0.7 l.5 KB"
/nove=="Vector: pBGK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.5%; Pred. No. 45;
Matches 103; Conservative 0; Mismatches 71; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGE
912 Medical Center Drive, Rockville, MD 20850, USA 7112 Medical Center Drive, Rockville, MD 20850, USA 7121: 301-838-584 Serial: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1.802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG326739.1 GI:34244005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays
Zea mays
                                                                                                                                                                                                                                                                  224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 20
CG326739
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                        d
                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                            Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
      δ
```

GSS 16-MAY-2003

DNA

830 bp

RESULT 21 CC331586/c LOCUS

```
CKI61968 1148 bp mRNA linear EST 05-DEC-2003 FGAS014551 Triticum aestivum FGAS: Library 4 Gate 8 Triticum aestivum cDNA, mRNA sequence. CKI61968 CKI61968.1 GI:38990698 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum (bread wheat)

Triticum aestivum

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Pooldeae, Triticeae, Triticum.

[ bases 1 to 1148]

Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D., Genswein,B., Graf,R., Gullck,P., Hrycan,L.D., Laroche,A., Links,M.G., McCarthy,E.L., Monrcy,A., Muzak,I., Nilson,D., Functional Genomics of Ablotic Stress In Wheat and Canola Crops Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 ACGGCAACGGCGCAACGAGTCCAACGCGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 Terechecesegacereareacesegacesececececeareaneresecencesean 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD Calde, Panicoideae, Andropogoneae; Zea.

1 (bases 1 to 830)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Coltek, R., Numberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 acácerrécadrecadedadacerecedadadedrecerecrecrecrededes 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 TGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACC
OGOBHISTV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0344C06, genomic survey sequence. CC331586 CC331586.1 GI:30800757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: sheared ends.

Location/Qualifiers

1. 830
/organism="Zea mays"
/mol type="genomic DNA"
/strain=B37"
/db xref="caxon:4577"
/clone="ZMNDMA0344C06"
/clone="ZMNDMA0344C06"
/clone="ZMNDMA034C06"
/clone="ZMNDMA034C06"
/clone="ZMNDMA034C06"
/clone="ZMNDMA034C06"
/clone="ZMO07"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 k
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 28; Length 830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.5%; Score 45.4; DB 28; Length Best Local Similarity 57.5%; Pred. No. 46; Matches 103; Conservative 0; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: TF
                                                                                                                                                             Zea mays
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
```

COMMENT

PEATURES

```
/closue type="seedling green leaf"
/lab host="Recoboulough"
/lab host="SOLR"
/lab host="Sol
                                    Pooldeas, Triticeae, Hordeum.

1 (bases 1 to 538)
Wing, R., Glose, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D.,
Wing, R., Glose, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D.,
Choi, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J.,
Choi, D.W., Fenton, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla6) seedling
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCGATCGGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCAC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 CGITCAIATCGGGCCIACCGCCITCCTCGGCTTGGGTGTTGTCGACAACAACAACGAACGG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eècectecectraceetcacectritercaaececeseaedactactractorcarcaa 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 rececrececerásce acercánica aceceáca de recece a dececeácica de contra d
spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.4%; Score 45.2; DB 10;
llarity 48.6%; Pred. No. 45;
Conservative 0; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublication University Genomics Institute Clemson University Genomics Institute Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="C116151 (Mla6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sub_species="vulgare"
db_xref="taxon:112509"
clone="HV_CED0007J02f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total hq bases = 199
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 462.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285
                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                         REFERENCE
                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                               Bioinformatics
University of Saskatchewan, Department of Computer Science
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatcon,
Saskatchewan, 57N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas ests@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [28, 831].
Plate: L48003 row: H column: 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /uz.ret="Laxou:350" / vactor: pure fate 8" / olone lib="Triticum aestivum FGAS: Library 4 Gate 8" / note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial parts (crown and leaf) of wheat cultivar Norstar during dehydration stress. 8 mRNA populations were combined before constructing the library. The first four come from removing plants from vermiculite (7 day old plants) and incubating them at 20°C on the bench without water for 1, 2, 3 and 4 days. The last four come from plants grown in soil in a growth chamber after watering is terminated. Four samplings were taken in a two week period; the first after wilting was observed and the last, two weeks later, consisted of live crown and stem tissue (lasf tissue was yellow and dead). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with Notl."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    538 bp. mRNA linear EST 23-OCT-2001
HVCDM5005 (Blumeria challenged) Hordeum vulgare seedling green leaf EST library
CDNA clone HV_CEb0007102f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 GGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAGCGAACGGCACGAGGTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 crecededrecedededecenteacedentrerederentesconstructadescae 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 ACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 crescencerearcesceceses de receses de consecuences es conseces de consecuences de 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435 AACGGGGTGTCGGCGGCGGTGTTCAGCAAGGAGCACCTGCTGGAGGAGCACGTGATGAGCGCG 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 TACGGCCACGCCGGCTTCGCCAAGCGCGGGGGGGCTACTTCCTCGTCAAGCCTGACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 CAACGCGTGGTCGGGAGCGCTCCGGCGGAAGTCTCGGCATCTCCACCGGCGACGTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 CATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCCAAGTCGGGCGGCACCGC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 14; Length 1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 47.1%; Pred. No. 49;
Matches 139; Conservative 0; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'mo]_type="mRNA"
'db xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE215641 -- BE215641.1 GI:8903169
               Contact: Wm L Crosby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 23
BE215641
```

DRIGIN

à 원 ठे qq ò 셤 ઠે 284

Gaps

ó

엄 ò 셤 à 쉼

à

```
Useroscope.

Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 BYRX cedex - FRANCE (B-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gsoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecot at ST library is named RPCI-98 and was constructed by partial Ecot RST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be content of Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
                                                                       brosophila melanogaster genome survey sequence TET3 end of BAC #BACR10516 of RPCI-98 library from Drosophila melanogaster (fruit AL054280 AL054280.1 GI:4931788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 GGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGACGACGCCACGAGTCC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || : :: :: :: || |::|| | : : : : :|| |:: :|| |: : :|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: :|| |: :|| |: :|| |: :|| |: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCGGTCGACGCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCCACCGTTCATATCG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 ATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGTACAG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSSCSBSSCSCCASSSRASGCSBSSSSSCSSVSCSMSGCMCAMSSASSSSSAGGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 SMSSSSACSASASSSGCSASSCVAACSSACAGSGASAGSSSSASGSCGAGSSSSAGGSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 AACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ĊSAVSSGAASSĠSASGCĊGCSSSSGĊSSCSSSSSMSCSSSSCSSSSGCSSVCSCSSCVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoā; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilae; Drosophila.
1. (bases 1 to 839)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.3%; Score 44.6; DB 29;
Best Local Similarity 15.9%; Pred. No. 66;
Matches 59; Conservative 150; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila mel/mol_type="genomic DNA"
db_xref="texon:7227"
/dlone="BACR10E16"
/clone="BACR10E16"
/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                            GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                705
                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
RESULT 25
CNS004NB
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPALISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS OF PORPHYRA YEZOENSIS (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE TAG FREQUENCY ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA linear EST 14-OCT-2003 sporophytes Porphyra yezoensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 Adeneacreecreeccecreeracerecercercareacerecececcecreeces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 ACGAGTCCAACGCGTGGTCGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGA 236
                                                                                                                                                                                                      CGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACGCGGATGGCGGAAGC 293
     174 GCCACGAGTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 ceccéectrecrescrercardaccecaeceaecescrerceceseresces as establicados de constantes de constantes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCGGGCAGGCGATGGCGATCGCGGCCAGATCCGATCGGGTGGGGGGTCACCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 TCATATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 crácicació accacica de desenta de contra d
                                                                                                   GOCOGACTGCCTTCGCCGCGACCCCTCCACCCCTTCTTCGTCTTCGCCGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porphyra yezoensis
Eukaryota, Rhodophyta, Bangiophyceae, Bangiales, Bangiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saga, N., Nakamura, Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 TAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="PFL024412 r"
/dev stage="sporophytes"
/clone_lib="Porphyra yezoensis TU-1 sporophytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Phycol. 39 (5), 923-930 (2003)
Content: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.3%; Score 44.8; DB 9; 47.0%; Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502 bp mRNA AU191977 Porphyra yezoensis TU-1 sporoph; cDNA clone PFL024al2_r 5', mRNA sequence AU191977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Porphyra yezoensis"
|mol_type="mRNA"
|strain="TD-1"
|db_xref="taxon:2788"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 502)
Asamizu,E., Nakajima,M., Kitade,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU191977.1 GI:31930158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphyra yezoensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGAACGCGC 475
                                                                                                                                                                                                                                                                                                                                                                                                                 GCTTAACGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porphyra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fabata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254
                                                                                                              345
                                                                                                                                                                                                           234
                                                                                                                                                                                                                                                                                                              405
                                                                                                                                                                                                                                                                                                                                                                                                                       294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 24
AU191977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
```

ö

584

524

ò d à g à 셤 ò g à

64

824

셤

```
BJ307565 Y. Ogihara unpublished cDNA library, Wh_yd Triticum aestrivum cDNA clone whydlip23 3', mRNA sequence.
BJ307565.1 GI:20116389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Triticum aestivum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
(Dases 1 to 496).
Ogihara, Y. and Mural, Rypiceae in Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 AGICICGGCAICICCACCGGCGACGIGAICACCGCGGTCGACGGCGCTCCGAICAACICG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       971
BX360624 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA Clone CS0DI072YL05 3-PRIME, mRNA sequence.
BX360624.1 GI:30376452
                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (Dases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol type="mine" current
/mol type="mine" current
/mol type="mine" current
/clone="cs0D1072XL05"
/clone="cs0D1072XL05"
/tissue type="Homo sapiens PlaCENTA COT 25-NORMALIZED"
/clone="lst strand cDNA was primed with a NotI-oligo(dT)
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 TCGGGTGGGGGTCACCCACCGTTCATATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 GTCGACAACAGCGCAACGCGCACGAGTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre Cedax - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4982.r
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO?ZCFO3NPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 10.2%; Pred. No. 71;
Matches 19; Conservative 112; Mismatches 56; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .1201
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum (bread wheat)
                                                                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 GCCACCG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   910 SSSSVSS 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 28
BJ307565/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
             DEFINITION
                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                       ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
//organism="MRNA"
/db_xref="taxon:9606"
/db_xref="csoCaP002XE11"
/clone="CsoCaP002XE11"
/clone="TYMUS"
/clone="TYMUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 05-MAY-2003
                                                                                                                                                                                                                                                                                                                      BX456467 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP002YE11
5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    978 MRGCGGGGGCCCGSCCCCCCCCCCCCGGCCGGGGGCSGCCCCGCGGGGGSGGCS 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCCACCGTTCATATCG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 GGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGAGTCC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 AACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         918 csccedececementececestes de contra de cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases I to 1200)

1. M.B., Gruber, C., Jessee, J. and Polayes, D.

Pull.length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Genoscope
Contract: Genoscope
Contract: Genoscope
Bp 191 91006 EVRY codex - France
Bp 191 91006 EVRY codex - France
Email: seqretégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Livitrogen. Contact : Feng Liang Email: filangelifetecen.com URL
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPO02AC06QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 ccgcgrccgataacticcagcrgrccagggrgggcagggatrcgccatrccgatcggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.3%; Score 44.6; DB 13; Length 1200; 40.2%; Pred. No. 71; tive 28; Mismatches 125; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ďq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1158 cceseccesecces 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX456467.1 GI:31032763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 CCGCGGTCGACGGCGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                 825 SVVASSCGAVV 835
                                                                     GGAACGIGACA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BX360624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 27
BX360624/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                  LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                          RESULT 26
BX456467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ⋧
```

ö

Gaps

```
BH189840 590 bp DNA linear GSS 19-OCT-2001 XXCC41TR ATXO Arabidopsis thaliana genomic clone ATXOC41, genomic survey sequence.
BH189840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Wiridiplantae; Streptophyta; Budicotts;
cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (base I to 590)
Kaul, S., Town, C.D., Bowman, C.L., Van Aken, S.E., Utterback, T.V.,
Feldblyum, T.V. and Fraser, C.M.
Survey sequencing of Arabidopsis thaliana BAC T2464
Unpublished (2001)
Other_GSS: ATXOC41FF
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fmax: 301-838-0208
Fmail: cdcown@tigr.org
From Wash. U contig 1142. Caution: the DNA in this BAC may be from some non-Arabidopsis source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 TCGACAACAACGGCAACGGCGCACGAGTCCAACGCGTGGTCGGGAGCGCTCCGGCGAA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 TOGACAACAACGGCAACGGCGCACGAGTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 resserresidenciares de anteres de contra d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia"
/db.xref="texton:3702"
/clone="ATXOC41"
/clone="ATXOC41"
/clone="ATXOC41"
/note="Wetcr: pHOS2; Site 1: BstX1; 2-3 kb sheared BAC
DNA inserted into pHOS2 usIng BstX1 linkers"
/mol_type="genomic DNA"
/#strain="columbia"
/db xref="taxon:3702"
/clone="ATXOC60"
/clone="ATXOC60"
/clone="Lb="ATXOC
/note="Weator: pHOS2; Site 1: BstXI; 2-3 kb sheared BAC
DNA inserted into pHOS2 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 GTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 AGATOGOCOTOGOCACOTOGOCATOATOACOGACTACOACTGOTGOAAAACOGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 CCCCGTCACCGCCGAAGCCGTCATCGCCCACCTCCACGCCAATGTCAGCATGG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 CCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCATCTCGG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 590;
                                                                                                                                                                                                                                                                                                                                                                                              Score 44.4; DB 28; Length 504; Pred. No. 64; 0; Mismatches 81; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.2%; Score 44.4; DB 28;
llarity 53.4%; Pred. No. 66;
Conservative 0; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH189840.1 GI:16302367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      =
=
=
=
                                                                                                                                                                                                                                                                                                                                                                                                        / Match
Local Similarity 53.4%;
nes 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seg primer: TR
Class: sheared ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 30
BH189840/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BH190076 504 bp DNA linear GSS 19-OCT-2001
ATXOC60TF ATXO Arabidopsis thaliana genomic clone ATXOC60, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301-838-3523
Fax: 301-838-3208
Faxi: 301-838-0208
Faxi: 301-838-0208
From Wash. U contig 1142. Caution: the DNA in this BAC may be from some non-Arabidopsis source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryoshyta; thaliana
Bukaryoshyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Viridiplantae; Streptophyta; endicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
I cosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

(bases I to 504)
Kaul,S., Town,C.D., Bowman,C.L., Van Aken,S.E., Utterback,T.V.,
Survey sequencing of Arabidopsis thaliana BAC 724G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397 decelaedecaaecedaligielelaedeceretreraelaaecedeceaedaedecerelee 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 TICCCGGCCGGCCCGGCGGAGCCGCCGGCGGTGCGTACCCCAGGTTCGTGTTCGAG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457 ecregadoroárca coracego a a desta caracidades de conserco do conservo de c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 GCGGCAAGTCTCGGCATCTCCACCGGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 AACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCGCGGTGACGTCATCTCG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGACCTGGCAAACCAAGTCGGGCGCGCACGCTACAGGGAACGTGACATTGGCCGAGG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 gactacatgadecteracerecececacaaetrceareacadeeaecceaeerreade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/culfivar="chinese Spring"
/culfivar="chinese Spring"
/db xref="taxon:4565"
/clone="whydlip23"
/tissue_type="spikelet at late flowering"
/tissue_type="spikelet"
/clone="peekes' scale 6"
/clone_lib="Y. Ogihara unpublished cDNA library, Wh_yd"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 GGTGTTGTCGACAACAACGGCAACGGCGCACGAGTCCAACGCGTGGTCGGGAGCGCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.2%; Score 44.4; DB 12; Length 496; Larity 49.2%; Pred. No. 64; Conservative 0; Mismatches 121; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive, Rockville, MD 20850, USA
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. :504
/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH190076.1 GI:16302878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other_GSSB: ATXOC60TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                             . .496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            survey sequence.
BH190076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity
117; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S:
Matches 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 29
BH190076/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
COMMENT
                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
```

셤 ò 셤 ò g ò ô

Gapa

.; 0

us-09-684-215b-3.rst

216 TOGGCTTCGACGTCATCGGCATGACCTCCCCGGAAGCCAAGCTCGCCCGCGAAGCCG 157

275 CCACCGGGATGGCGGACGGCTTAACGGGCATCATCCCGGTGACGTCATCTCGG 328

Search completed: April 30, 2004, 07:40:32 Job time : 2052 secs

Dp

ĕ

```
Human pro
DNA encod
Human RA1
                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia
DNA encod
Chlamydia
                                                 Lung tumo
Ra12-P775
Human /M.
Prostate
Ra12- P77
                                                                                                                           Human pro
DNA encod
Human lun
Lung canc
Ra12/N-te
                                                                                                                                                                                      Human lun
Lung tumo
DNA encod
                                                                                                                                                                                                                             Human col
Human RA1
DNA encod
Human Ra1
                                                                                                                                                                                                                                                                               Lung canc
Ra12-P501
Human /M.
Prostate
Ra12-P501
Prostate
                       Ra12/C-te
Human lun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide encoding a prostate-specific protein, for diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                   DNA encod
                                                                                                               Prostate
Lung
          Abk27798 Abk27798 Abd149257 Abd149257 Abd28443 Add28443 Acc5556 Abd14284 Acc956512 Acc35676 Abd28441 Abk33917 Acc35961 Acc35961 Acc35961 Acc35961 Acc35961 Acc35961 Acc35961 Acc35961 Acc35688 Add1531 Add16321 Add16331 Add16331 Add16331 Add16332 Acc3588 Add16331 Add16331 Add16331 Add16332 Add
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harlocker SL, Jiang Y, Reed
Retter MW, Stolk JA, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, prostate cancer, prostate-specific, diagnosis, vaccine, cytostatic, gene therapy, metastasis, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                           ADB14284
ABK39768
ACA12097
                                                                                                                                                                                                                                                                                                AAH93917
AAS64153
ACA59961
ABL95524
ACC95688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ra12-P510S-C construct cDNA sequence.
                                                                                                                                                                  ACA03283
ABL49256
                                                                                                                                                                                                                    ABK69714
ABZ33699
                                                                                                                                                                                                                                             ADB67590
                                                                                                                                                                                                                                                                                  ACA03290
                                                                                                                                                                                                                                                                                                                                                                                                                              AAH56341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH56267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2001; 2001WO-US001574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH93896 standard; cDNA; 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JAN-2000; 2000US-00483672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu J, Dillon DC, Mitcham
Kalos MD, Fanger GR, Day
Wang A, Meagher MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2001 (first entry)
 WPI; 2001-425873/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
WO200151633-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2001
 AAH93896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH93896
ID AAH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
  Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgnz_1/USFTO=p0.model -DEV=xlh
-Q=/cgnz_1/USFTO=p0.model -DEV=xlh
-D=N Geneseq_295ano4 -OPMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MARRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFYT=pto -NORN=ext -HEAPPIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09684215_@CGN_1 1_819_@runat_29042004_061304_13179 -NCPU=6 -ICPU=3
-NO_MARP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOKE+10 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREAPS=1 -XGAPEXT=0.5 -FGAPEN=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aah33896 Ra12-P510
Aas64132 Human /M.
Aca59940 Prostate
Ab195503 Ra12-P51
Acc95667 Prostate
Adb4272 Human pro
Acs9769 DNA encod
Aca12098 Human lun
                                                                                       April 29, 2004, 20:30:12; Search time 364.096 Seconds (without alignments) 1493.479 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                         653
1 TAASDNFQLSQGGQGFAIPI.....QTKSGGTRTGNVTLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                   nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                          3373863 segs, 2124099041 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH93896
AAS64132
ACA59940
ABL95503
ACC95667
ADB14272
ABK39769
                                                                                                                                                                                                            ....
                                                                                                                                                                                             BLOSUM62
Xgapop 10.0, Ygapext (
Ygapop 10.0, Ygapext (
Fgapop 6.0, Fgapext (
Delop 6.0, Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Geneseq_29Jan04:*
| Geneseq_1980s:*
| Geneseqn1980s:*
| Geneseqn2000s:*
| Geneseqn2001s:*
| Geneseqn2001s:*
| Geneseqn2001s:*
| Geneseqn2003s:*
| Geneseqn2003s:*
| Geneseqn2003s:*
| Geneseqn2003s:*
| Geneseqn2003s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ü
                                                                                                                                                                                                                                                                                                                             seg length: 0
seg length: 200000000
                                                                                                                                             US-09-684-215B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6675
675
675
822
822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                           Minimum DB &
Maximum DB &
                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 1 4 1 1 9 1 2
                                                                                           Run on:
```

```
The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (II), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) area used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for wonitoring the progression of cancer in a patient. (I) and (II) can be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93394 and AAM01115 to AAM01318 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gressandescreecesconagererescarerecesconescones and 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gergacercarcrosergaccroscaaaccaaercesecesecececeraceaesaacere 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACGGCCCCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLygLeuProThrValHisIleGlyProThr
ij
monitoring and treating prostate cancer in a patient and for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; prostate cancer; ss; cytostatic; immunostimulant; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human /M. tuberculosis Ra12 fusion protein RA12-P510S-C cDNA
                                                                                                                                                                                                                                                                                                                   Seguence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                  675
128
0
0
                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-18 (1-128) x AAH93896 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405
                                              Claim 8; Page 492-493; 543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrieuAlaGluGlyProProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               382 ACATTGGCCGAGGGACCCCCGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS64132 standard; cDNA; 675
                                                                                                                                                                                                                                                                                                                                                             2.71e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                      the present invention
                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2002
                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS64132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS64132
ID AAS6
XX AAS6
XX DT 29-J
DT 29-D
DE Huma
XX Huma
XX Huma
XX Homc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
```

```
The invention relates to isolated prostate-specific polynuclectides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynuclectides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynuclectide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonuclectide is useful for detecting cancer. The prostate specific polynuclectide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCTTCCTCGGCTTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGAGTCCAACGCGTG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThralaalaseraspasnPheGlnLeuserGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human prostate-specific polypeptides and polynucleotides useful
the diagnosis and treatment of cancer, especially prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                               Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                           Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-684-215B-18 (1-128) x AAS64132 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 17; Page 532; 579pp; English.
                                                                                                                                                                                                    13-UTN-2000) 2000US-00593793.
27-UTN-2000) 2000US-00693793.
29-AUG-2000) 2000US-00635215.
29-AUG-2000) 2000US-00651236.
06-SEP-2000) 2000US-00657279.
02-OCT-2000) 2000US-00679426.
10-OCT-2000) 2000US-00679416.
Microbacterium; tuberculosis.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.716-58
653.00
100.00%
100.00%
                                                                                                                             27-MAR-2001; 2001WO-US009919
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639232/73.
                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAU69899
                                                                WO200173032-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                              04-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142
                                                                                                                                                                                                                                                                                                                                                                                                 Fanger (
Li SX,
                                                                                                                                                                                                                                                                                                                                                                                Xu J,
 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

40

20 81 9

```
GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
           GTCGGGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC 261
                                      100
                                                         321
                                                                                                Gercacercarcredereacereaceaaaceaagregeegeegeegeacereaceaagaacere 381
80
                                                   GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGAACGCGCTTAACGGGCATCATCCC
                                       AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                        Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA; prostatic acid phosphatase; PAP; prostate specific membrane antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalos MD;
Carter D;
Hural J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Pw. Houghton RL, Y De Bassolscv, Foy TM;
                                                                                                                                                                                                                                     Prostate cancer therapy associated cDNA #647.
                                                                                                                              ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                   ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                            ACAS9940 standard; cDNA; 675 BP
                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-1999; 99US-0157455P.
04-OCT-2000; 2000US-00679272.
28-MAR-2001; 2001US-00822827.
                                                                                                                                                                                                                                                                                                                                                                    29-JUN-2001; 2001US-00895793
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOUGHTON R L.
Y DE BASSOLS C V.
                                                                                                                                                                                                                                                                                                                                                                                                                             XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JIANG Y.
KALOS M D.
RATOS M D.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HURAL J.
MCNEILL P D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-245062/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOY T M.
                                                                                                                                                                                                                                                                                                                              US2002192763-A1.
                                                                                                                                                                                                                                                                                         PSMA; gene; ss.
                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Au J, Dillor
Fanger GR, F
Li SX, Wang
Mcneill PD,
                                                                                                                                                                                                                    10-JUN-2003
                                                                                                                                                                                                                                                                                                                                                 19-DEC-2002
                                                                                                                                       382
                                                                                                                                                                                                  ACA59940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HOUG/) H
(DBAS/) N
(FOYT/) H
                                                                                                 322
                                                                                                                                                                                                                                                                                                                                                                                                                             (XUJJ))
(MILL))
(MILL))
(HARL)
(HARL)
(AIAN)
(AIAN)
(RETT)
(STOL)
(STOL)
(CART)
(LISX)
(HEPL)
(HURD)
                   202
                                       81
                                                         262
                                                                             101
                                                                                                                   121
                                                                                                                                                          RESULT
                                                                                                                                                                    ACA5994
                                                                                                                                                                              g
                                                  8 8
                                                                                            a
                                                                                                            à
              g
                                    ð
```

```
The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated cNNA. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at sequence.html?DocID=US20020192763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381
Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 GTCGGGAACGCTCCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyAspvalileServalThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 GGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGGCACGCGTACAGAGAACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 Aceccecetrocaracriccaerererecaeereeecaeecaeearreecarreeeare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 gacgececrecearcaacregeceacedeargeceacedeacecerraacegecareace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                      Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                        Ral2- P510S-C construct cDNA sequence SEQ ID NO 822.
                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                    Example 17; SEQ ID NO 822; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215B-18 (1-128) x ACA59940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL95503 standard; cDNA; 675
                                                                                                                                                                                                                                                                                                                                                                    2.71e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-2003
19-JUL-2002
                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL95503;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL95503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XXXXXXXXXXXXXXXX
   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    슝
```

```
New prostate-specific proteins and genes, useful in gene therapy, particularly for stimulating an immune response in a patient, or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                   141
                                                                                                                                                                                                                                                                                                                                                                                                                               201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                     40
                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA; Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS; Carrer D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J; Mcneill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y; Deng T;
                                                                                                                                                                                                                                                                                                                       82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                                                                                                                                                                                 22 ACGGCCCCCCCCCCCATACTTCCCACTCTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                        GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ValGlySerAlaDroAlaAlaSerLeuGlyIleSerThrGlyABpValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 GTCGGGAGCGCTCCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyAspValileSerValThrTrpGlnThrLy8SerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                            ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                               41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                             142 eccriccredecringeroricisce Acaacaa ce accaece co con conservante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic, gene therapy, prostate-specific protein, PSP; human; immune response; prostate cancer; ss.
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostate tumour specific cDNA sequence SEQ ID 822
  Matches:
Conservative:
Mismatches:
Indels:
                                                                                              Gaps:
                                                                                                                                            US-09-684-215B-18 (1-128) x ABL95503 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2001; 2001US-00852911.
29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC95667 standard; cDNA; 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAY-2002; 2002WO-US014753.
  653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-167130/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200289747-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC95667;
                                                                                                                                                                                            Н
                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC95667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRAKA X PRAKA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      유
                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                ठे
                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y,
Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G; 126 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 17; SEQ ID NO 822; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; 190
                                                                                                                                                                                                                                     25-FEB-1997; 97US-000606099.
01-AUG-1997; 97US-000904804.
10-FEB-1998; 98US-00020956.
25-FEB-1998; 98US-00015453.
23-SEP-1998; 98US-00015453.
23-SEP-1998; 99US-00015423.
15-JAN-1999; 99US-00232149.
15-JAN-1999; 99US-00232149.
12-NOV-1999; 99US-00352646.
12-NOV-1999; 99US-00439313.
12-NAR-2000; 2000US-0043667.
27-JAN-2000; 2000US-00568100.
12-MAX-2000; 2000US-0053793.
13-JUN-2000; 2000US-0053793.
13-JUN-2000; 2000US-0053793.
13-JUN-2000; 2000US-0053793.
13-JUN-2000; 2000US-0053793.
10-AUG-2000; 2000US-0053793.
10-AUG-2000; 2000US-0053793.
10-AUG-2000; 2000US-0053793.
10-AUG-2000; 2000US-0053793.
                                                                                                                                                                                                 2001US-00759143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 675 BP; 162 A; 197
       Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-255649/30.
                                                                                                   US200202248-A1
                                 Homo sapiens
Chimeric.
                                                                                                                                                                                                 12-JAN-2001;
                                                                                                                                                 21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DILL/)
(MITC/)
(HARL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JIAN/)
(KALO/)
(FANG/)
(RETT/)
(STOL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (VEDV/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LISX/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HEPL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (XCCX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKEI/)
```

675

Length:

2.71e-58

Alignment Scores: Pred. No.:

02-OCT-2003

```
The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyAspvallleServalThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC 321
                                                                                                                                                                                                                                                                                                                                                                                                 22 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGGCAGGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlapheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
prostate cancer in a patient, as well as for diagnosing prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; prostate specific cDNA; cytostatic; immunostimulant; gene therapy; call therapy; vaccine; T-cell epitope; class in anjor histocompatibility complex allele; MHC; prostate cancer; tumour; antigen presenting cell; gene; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                               ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyBheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValGlySerAlaProAlaAlaSerLeuGly11eSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate specific protein P510S-RA12 construct C cDNA.
                                                                                                                                                                                     Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                Example 17; Page 601-602; 691pp; English
                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                 US-09-684-215B-18 (1-128) x ACC95667 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB14272 standard; cDNA; 675
                                                                                                                                                                                                                                    2.71e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                            illustrate the invention
                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003185830-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2003
                                                                                                                                                                                                                        Alignment Scores:
                  in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB14272;
                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric
                                                                                                                                                                                                                                                                                                       Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
ADB14272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Б
                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

```
The invention relates to an isolated polypeptide comprising no more than content and acids of ADB13563 comprising a sequence ADB14487. The peptides comprise a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (WHC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific companion one of 648 disclosed as new. Also included are nucleic acids encoding the proteins and peptides, expression vectors, a host cell tragment) that specifically binds to the protein or peptide, detecting cragment) that specifically binds to the protein or peptide, detecting the presence of a cancer in a patient (comprising contacting a patient cample with a binding agent that binds to the protein or peptides or a polypeptide to a predetermined cutcomparing as ADB13588, detecting the amount of polypeptide to a predetermined cutcomparing the amount of polypeptide to a predetermined cutcomparing the peptides or proteins, stimulating or expanding T cells specific for a tumour protein comprising or cancer; a fusion protein comprising contacting T cells specific for a tumour protein comprising contacting T cells specific for a tumour protein comprising contacting T cells specific for a tumour protein comprising contacting T cells or composition comprising the peptides, or composition comprising the peptides, or composition comprising the peptides or composition comprising cluster of differentiation (CD4+) and/or CD8+ T cells in the peptides or antigen presenting cells that express (the peptides so that the T cells proliferate, and administering the composition comprised contacting the peptides or antigen presenting cluster of differentiation (CD4+) and/or CD8+ T cells in the peptides or antigen presenting cluster of differentiation (CD4+) and/or CD8+ T cells to the patient. The peptides (or an oligonucleotide contact in a patient and really proliferate, and administering the peptides or composition contacting a so that that thy the peptides (or an oligonucleotide 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 17; Page; 101pp; English.
                                                                                                                                                                                                                                                                                                                      14-JAN-2000; 2000US-00483672.
27-MAR-2000; 2000US-0058657.
29-MAY-2000; 2000US-00586100.
12-MAY-2000; 2000US-00558140.
13-JUN-2000; 2000US-00558142.
29-AUG-2000; 2000US-00651236.
29-AUG-2000; 2000US-00651236.
29-AUG-2000; 2000US-00651236.
10-CCT-2000; 2000US-00651236.
                                                                                                         97US-00904804.
98US-00020956.
98US-00115453.
98US-00159812.
99US-00288946.
99US-00352616.
99US-00435819.
                                            2002US-00294025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ku J, Stolk JA, Kalos MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-756193/71.
P-PSDB; ADB14275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                              13-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer
```

```
antigen-presenting cells expressing the nucleic acid, are used to stimulate or expand T cells specific for a tumour protein. The peptides, nucleic acids, antibodies, fusion proteins, T cell populations or antigen presenting cells are used to etimulate an immune response or treat prostate cancer in a patient. The present sequence is a cDNA encoding a fusion protein comprising a prostate specific protein. Note: Except where otherwise indicated, the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030185830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGCACGCGTACAGGGAACGTG 381
                                                                                                                                                                                                                                                                                                                                                                                                                82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GICGGGAGCGCICCGGCGGCAGTCTCGGCATCTCCACCGGCGACGTGATCACGGCGGTC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC 321
                                                                                                                                                                                                                                                                                                                                                                                     40
                                                                                                                                                                                                                                                                                                                                                                                                                                          AlapheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                               ACGCCCCCCTCCCATAACTTCCCACTGTCCCAGGGTGGGCAGGGATTCCCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCTTCCTCGGCTTGGGGTGTTGTCGACAACAACGGCAACGGCGCACGAGGTCCAACGCGTG
                                                                                                                                                                                                                                                                                                                                                                                     GlyGlnAlaMetAlaIleAlaGlyGlnIleLySLeuProThrValHiSIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                              ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lung tumour protein P801P ORFS and Ra12 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour; cancer; I cell; immune response stimulator; cytostatic
                                                                                                                                                BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                            675
128
0
0
0
                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                  (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                  US-09-684-215B-18 (1-128) x ADB14272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUL-2001; 2001WO-US022058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK39769 standard; cDNA; 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUL-2000; 2000US-00614124
                                                                                                                                                                                          2.71e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                     Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200204514-A2
                                                                                                                                                                                             Pred. No.:
Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
Synthetic.
                                                                                                                                                   Sequence 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAY-2002
                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                Н
                                                                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                               41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK39769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
ABK39769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8888888888888
                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                à
```

```
The invention describes an isolated polymucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein containing the presence of a cancer in a patient. A composition a lung cancer in a patient. The polympeptide is useful for treating a lung cancer in a patient. The polympeptide is useful for treating a rolls from a biological sample. The polymorleotide is also useful as probe or primer to detect the level of many according a tumour protein. This sequence encodes a lung tumour associated protein or protein. Fragment, described in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
                                                                                                                                                                     Ą;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 eccircicederregererereseacaacaacedeecececedadeecere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCAGGCGATGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGGCGACGTGATCACGCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyaspvalileServalThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 ACGGCCCCCGTCCCGATAACTTCCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                    Mcnabb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                               Novel polynucleotide encoding a lung tumor polypeptide useful for stimulating and/or expanding T cells specific for a tumor protein
                                                                                                                                                   Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS,
Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 822 BP; 146 A; 281 C; 270 G; 125 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                             Example 8; SEQ ID NO 1862; 223pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-684-215B-18 (1-128) x ABK39769 (1-822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrLeuAlaGluGlyProProAla 128
29-AUG-2000; 2000US-00651563.
08-SEP-2000; 2000US-00658824.
26-SEP-2000; 2000US-00671325.
06-OCT-2000; 2000US-00677419.
30-OCT-2000; 2000US-00702705.
13-DEC-2000; 2000US-0074657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.44e-58
653.00
100.00%
100.00%
                                                                                                                                                        Wang T, Watanabe Y,
Marnerakis M, Carter
                                                                                                                            (CORI-) CORIXA CORP
                                                                                                                                                                                                                    2002-164634/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                    WPI; 2002-164634,
P-PSDB; AAU85587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Si
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
    ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                상
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
The invention relates to a polymucleotide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in protein comprising a sequence selected from any of the 14 sequences mentioned in complement of S1, sequences consisting of at least 20 contiguous residues of S1, sequences that hybridise to S1, sequences having 75%, preferably CC obly identity to S1, or degenerate variants of S1. Also included are an isolated polypeptide (comprising a sequence (S1) selected from any one of the 4 amino acid sequences mentioned in the specification, a sequence corrected by the polymucleotide, or sequence shaving at least 70%, control sequence encoded by the polymucleotide, or sequence by the polymucleotide, or sequence and the specification, and sequence a host cell transformed or transfected with corrected by the polymucleotide, or a sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that the vector, a fusion protein comprising the polymptide, detecting the presence of a cancer of a funder or protein (comprising to the polypeptide, and the polymucleotide, protein conditions, stimulating and/or expanding T cells specific for a tumour conditions, stimulation and/or expansion of T cells) and inhibiting the development of a cancer in a patient with the polymucleotide, protein or antigen presenting cells, under conditions and for a time sufficient comprision contacting cells that express the polymucleotide, protein or antigen presenting cells, under conditions and for a time sufficient consistence administering to the patient an effective amount of the patient. The polymucleotide, protein or a patient. The polymucleotide, protein or a patient. The polymucleotide, protein or presenting cells, and thus inhibiting the development of a cancer in the patient. The patient is and thus inhibiting and a patient, and patient is a patient, and patient isu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang T, Switzer AP, Mcneill PD;
                                                                                                                                                                                                                Human lung cancer protein L801P ORF5/Ra12 fusion protein cDNA.
                                                                                                                                                                                                                                                          Human, lung cancer; ss; lung tumour; cytostatic; vaccine;
T cell expansion; CD4; CD8; RA12; gene.
382 ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang A,
                                                                                 вР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Page; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAY-2001; 2001US-00849626.
                                                                                 ACA12098 standard; cDNA; 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-2000; 2000US-00736457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fanger GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BANG/) BANGUR C S.
(FANGE) FANGER G R.
(WANG/) WANG A.
(WANG/) WANG T.
(SWIT/) SWITZER A P.
(MCNE) CLAPPER J D.
                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-352750/33.
P-PSDB; ABU69562.
                                                                                                                                                                                                                                                                                                                                                                                             JS2002197669-A1
                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                        06-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                          26-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bangur CS,
                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                              ACA12098;
                                                            ACA12098
                                                                                                       පු
```

```
treating a cancer in a patient (particularly lung cancer). The oligonucleotide is useful for determining the presence of a cancer in a patient. The protein and oligonucleotides are useful in pharmaceutical compositions, e.g. vaccines. The polymucleotide is also useful as a probe or primer for nucleic acid hybridisation, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polymeptides and proteins in tumour cells. An amplified portion of the polymeptides and proteins in tumour cells. An amplified portion of the library. The present sequence encodes a fusion protein of human RAL2 with the protein product of a cDNA (full length, extended or partial) isolated from a library derived from lung tumour/cancer cells. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 GICGGGAGCGCTCCGGCGGCAAGICTCGGCATCTCCACCGGCGACGTCACCGCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 ASDGIVALAPTOILEASUSSEVALATHTALAMETALAASDALALEUASUGIVHISFIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 Aceeccecerranacticaererceaeereeeeaeeearreecatreeere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLySLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATTCGGGGCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 GCCTTCCTCGGCTTCGGGTTCTCGACAACAACGGCAACGGCGCACGAGCGACCAACGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 GACGGGGTCCGATCAACTCGGCCACGGGATGGCGGAGACGCGCTTAACGGGCATCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 GlyaspvalileServalThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyBheAlalleProl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene; ds
                                                                                                                                                                                                                                                            Sequence 822 BP; 146 A; 281 C; 270 G; 125 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                             8
7
7
8
0
0
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lung cancer therapyand diagnosis associated DNA #5.
                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-18 (1-128) x ACA12098 (1-822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                              3.446-58
653.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACA03284 standard; DNA; 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002172952-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACA03284;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ଟ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
```

322 GGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGCGTACAGGGAACGTG 381

ThrieuAlaGluGlyProProAla 128

121

```
The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polynucleotide associated with the compositions and methods for the therapy and diagnosis of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide, useful for preparing a composition for treating inhibiting development of cancer, e.g. lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                 Henderson RA, Wang T, Watanabe Y, Johnson JC, Retter MW;
Durham M, Carter D, Fanger GR, Vedvick TS, Bangur CS, Mcnabb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 822 BP; 146 A; 281 C; 270 G; 125 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 8; SEQID NO 1862; 82pp; English
                        30-JUN-1999; 99US-00346492.

15-OCT-1999; 99US-004466867.
30-DEC-1999; 99US-00466867.
30-DEC-1999; 99US-00466867.
30-DEC-1999; 99US-00476300.
C6-MAR-2000; 2000US-00519642.
27-APR-2000; 2000US-00519642.
27-APR-2000; 2000US-0054606.
25-AUG-2000; 2000US-0058184.
11-JUL-2000; 2000US-0058184.
11-JUL-2000; 2000US-0058184.
29-AUG-2000; 2000US-0058184.
26-SEP-2000; 2000US-00581824.
26-SEP-2000; 2000US-00571419.
30-OCT-2000; 2000US-00571419.
33-OCCT-2000; 2000US-00571419.
33-DEC-2000; 2000US-00702705.
                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-328427/31.
```

or

Alignment Scores:

ASPGIVALAPROILEASNSERALATHRALAMETALAASPALALEUASNGIVHISHISPRO 100 GlyAgpvallleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAgnVal 120 22 ACGGCCCCCCCCCCATAACTTCCCAGCTGTCCCAGGGTGGCAGGAATTCCCCATTCCCATC 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVallleThrAlaVal 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyPheAlaIleProIle 877 000 000 000 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-684-215B-18 (1-128) x ACA03284 (1-822) 3.44e-58 653.00 100.00% 100.00% Percent Similarity: Best Local Similarity: 262 81 Query Match: DB: à 8 8 8 à a g ð à ò

201

9

40

81

261

80

Sequence 894 BP; 207 A; 269 C; 237 G; 181 T; 0 U; 0 Other;

Length: Matches: Conservative:

3.8e-58 653.00 100.00%

Score: Percent Similarity:

```
The invention relates to an isolated polymucleotide (I) encoding a polypeptide (II) comprising at least a portion of a colon tumour protein. C polypeptide (II) comprising at least a portion of a colon tumour protein.

(I), (II) and antibody (III) to (II) or antigen presenting cells expressing (I) is useful for stimulating and/or expanding T cells or specific for a tumour protein, by contacting T cells with (I), (II) or antigen-presenting cells that express (I), under conditions and for a cime sufficient to permit the stimulation and/or expansion of T cells.

(I), (II), or antigen presenting cells that express (II) are useful for treating colon cancer in a patient by incubating CD4+ and/or CD8+ T cells (I), (II) or antigen presenting cells that express (II), such that T cells proliferate, and administering to the express (II), such that T cells proliferate, and administering to the express (II), such that T cells proliferate, and administering to the concines and pharmaceutical compositions for prevention and treatment of colon malignancies and for the diagnosis and monitoring of such cancers.

(I), (II) or (III) is useful for detection, diagnosis and/or therapy of human colon cancer. (I) is useful as a probe or primer for nucleic acid hybridisation, and in the dessign and preparation of ribozyme molecules colon malignation of (II) in tumour cells. ABK27864-ABK27807 crepresent novel human colon cancer coding sequences and primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated polynucleotide encoding a polypeptide comprising a portion of colon tumor protein, useful for detection, diagnosis and therapy of human colon cancer.
                                                                                                                                                                                                                                    cell expansion; tumour; EST; gene;
                                                                                                                                                                                            Human colon cancer expressed sequence tag, Seq ID no 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clapper JD, Wang A, Secrist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 215-216; 220pp; English.
382 ACATTGGCCGAGGGACCCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUN-2000; 2000US-0210821P.
18-DEC-2000; 2000US-0256571P.
10-MAX-2001; 2001US-0290240P.
                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-2001; 2001WO-US018577
                                                                               ABK27798 standard; cDNA; 894
                                                                                                                                                           09-APR-2002 (first entry)
                                                                                                                                                                                                                                    Human; colon cancer; T expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jiang Y, Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-139708/18.
P-PSDB; AAU81532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                        WO200196390-A2.
                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                              20-DEC-2001
                                                                                                                       ABK27798;
                                              RESULT 10
                                                              ABK27798
```

```
ASPGIVALAPTOILEASDSETALATHTALAMELALAASPALALEUASDGIVHISHISPTO 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141
                                                                                                                                                                                                                                                                                                                                                                                 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                          40
                                                                                                                                                                                         81
                                                                                                                                         ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyBheAlalleProlle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                   GGGCAGGCGATGGCGATCGCGGGCCAAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                                                                                                                                                                                                                                                                                                41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                 ValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspVal1leThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                              GCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGCCAACGGCGCACGAGGTCCAACGCGTG
                                                                                                                                                                                                                                          GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ral2/C-terminal portion of L763P fusion polynucleotide SEQ ID NO:353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Henderson RA;
Fanger GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mang T, Wang A, Skeiky YAW, Li SX, Kalos MD,
Mcneill PD, Fanger N, Retter MW, Marnerakis M,
Vedvick TS, Carter D, Watanabe Y, Peckham DW;
Mismatches:
Indels:
Gaps:
                                                                                              (1-894)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrieuAlaGluGlyProProAla 128
                                                                                              (1-128) x ABK27798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-2000; 2000US-00606421.
02-AUG-2000; 2000US-00639940.
21-AUG-2000; 2000US-00641597.
15-SEP-2000; 2000US-00662786.
09-OCT-2000; 2000US-00685696.
12-DEC-2000; 2000US-0077705.
07-MAY-2001; 2001US-00850716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL49257 standard; cDNA; 900
  100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-090513/12.
P-PSDB; ABB75000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lung tumoun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200200174-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUN-2001;
                                                                                                   US-09-684-215B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang T,
Mcneill
                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                   142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1 ABIL 4925; 1 ABIL 4925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \dot{\delta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                  g
                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                      ठ
                                                                                                                                              8
```

```
100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyAspVall1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; lung tumour; cytostatic; gene therapy; vaccine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Greesekacecreesesekackeresekarereekekacakekarekeereeke 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381
                                                                                                                                                                                                                                                                                                                                                                                                   141
                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
                                            The present invention describes human lung tumour proteins. Human lung activities and polymucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polymucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 gacgececrocoarcaacrococcacecarocogacococcraaacococarcaroco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 GGGCAGGCGATGGCGGGCCAGATCCAGCTTCCACCGTTCATATCGGGCCTACC
                                                                                                                                                                                                                                                                                                                                        22 ACGGCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                            GlyClnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                             41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCAACGCGCACGAGGCCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                            1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                         C; 246 G; 196 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lung cancer associated DNA sequence SEQ ID NO:353
                                                                                                                                                                                                             900
1128
0
                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                   US-09-684-215B-18 (1-128) x ABL49257 (1-900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                                                            3.83e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABQ92443 standard; DNA; 900
                                                                                                                                                                          Sequence 900 BP; 219 A; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200247534-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-2002
                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                         142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   සි දි
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
#X&XCCCCCCCCXX
                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                          ∂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ठ
```

treating

Polynucleotides encoding lung tumor polypeptides, useful for

cancer or stimulating an immune response

lung

2 00:20:70

моп мау

Claim 1; Page 333-334; 374pp; English

12-DEC-2000; 2000US-00735705. 07-MAY-2001; 2001US-00850716. 28-JUN-2001; 2001US-00897778.

30-NOV-2001; 2001WO-US047576

(CORI-) CORIXA CORP.

Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA; Mcneill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS; Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;

WPI; 2002-583465/62. P-PSDB; ABP61920.

Novel lung carcinoma polynuclectide sequences and polypeptides encoded the polynuclectides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer.

ģ

Claim 8; Page 340-341; 381pp; English.

The present invention describes isolated human lung carcinoma polymucleotides (I) and polymeptides (II). (I) and (II) have cytostatic polymucleotides (I) and polymeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating the used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of sample with the oligonucleotide of electric oligonucleotide and comparing the prodetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to ABQ92192 represent sequences used in the exemplification of the present Invention

Sequence 900 BP; 219 A; 239 C; 246 G; 196 T; 0 U; 0 Other;

900	0	0	0	0
Length: Matches:	Conservative:	Mismatches:	Indels:	Gabs:
3.83e-58 653.00	100.00%	100.00%	100.00%	
Alignment Scores: Pred. No.: Score:	Percent Similarity:	Best Local Similarity:		

US-09-684-215B-18 (1-128) x ABQ92443 (1-900)

100 81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 262 GACGGCGCTCCGATCAACTCGGCCACGGCGATGGCGGACGCGCTTAACGGGCATCATCCC 101 쉱 g ò g & 엄 ò 셤 ò ò

```
tumour protein L763P C-terminal/Ral2 fusion DNA.
                                                                                                                  cancer; lung cancer; gene therapy; vaccine; human; lung squamous cell carcinoma; gene; ss; ral2.
18-MAR-1998; 98US-00040802.
27-JUL-1998; 98US-00123912.
22-DEC-1999; 99US-00221107.
02-ARR-1999; 99US-00286479.
17-DEC-1999; 99US-00466396.
10-JAN-2000; 99US-00466396.
10-JAN-2000; 2000US-00460884.
22-FEB-2000; 2000US-00542615.
28-JUN-2000; 2000US-005608421.
22-ANG-2000; 2000US-005608421.
23-AUG-2000; 2000US-005608940.
21-AUG-2000; 2000US-005639940.
21-AUG-2000; 2000US-00563997778.
                                                  BP.
                                                                                                                                                                                              30-NOV-2001; 2001US-00007700
                                                  ADA28443 standard; cDNA; 900
                                                                                   20-NOV-2003 (first entry)
                                                                                                                                                              US2003064947-A1.
                                                                                                                                              Homo sapiens.
                                                                                                                                                                              03-APR-2003.
                                                                   ADA28443;
                                                                                                     Lung
                                                    셤
```

The invention describes isolated polynucleotides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer. A new isolated polynucleotide comprises: any of the 22 fully defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above; at least 10 contiguous residues of the nucleotide sequences cited above; a sequence that hybridise to any of the nucleotide sequences under highly stringent conditions; a sequence that is at least 75 or 90% identical to the above nucleotide sequences; or degenerate variants of the above the above nucleotide sequences. The composition and methods are useful in diagnosing, preventing and/or treating cancer, particularly lung cancer, in gene therapy and in vaccines. This sequence encodes a fusion protein of human lung tumour protein L673P C-terminal and Ral2. New isolated polynucleotides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer. Claim 8; Page 253; 296pp; English.

Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA; Mcneill PD, Panger N, Retter MW, Durham M, Fanger GR, Vedvick TS; Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;

(CORI-) CORIXA CORP.

WPI; 2003-540798/51. P-PSDB; ADA28444.

Seguence 900 BP; 219 A; 239 C; 246 G; 196 T; 0 U; 0 Other;

```
RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGGGGGCGCGTACAGGGAACGTG 381
                                                                                                                                                                                                                                                                                                             141
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gregoracidente de de la contra del la contra della contra
                                                                                                                                                                                                                                                                                                                                                                                      201
                                                                                                                                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                            40
                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                     20
                                                                                                                                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosing,
use in
                                                                                                                                                                                                                                                                                                                                                                              Aceeccecerccearaacriccaecrerccaeeereeecaecaeariccccarrccarc
                                                                                                                                                                                                                                                                            GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                             GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC
                                                                                                                                                                                                                                                                                                                                                    AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                           ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                     ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide encoding a prostate-specific protein, for monitoring and treating prostate cancer in a patient and for vaccines.
                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; prostate-specific;
cytostatic; gene therapy; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ral2-P775P-ORF3 construct cDNA sequence.
                                                                                                                                                                 (1-900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 ACATTGGCCGAGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 搱.
                                                                                                                                                                 JS-09-684-215B-18 (1-128) x ADA28443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             년
유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH93905 standard; cDNA; 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JAN-2000; 2000US-00483672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2001; 2001WO-US001574
                                 3.83e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu J, Dillon DC, Mitcham Kalos MD, Fanger GR, Day Wang A, Meagher MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-425873/45.
                                                                      ent Similarity:
Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200151633-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2001.
                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322
                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                      41
                                                                                                                                                                                                                                                                                                                                                                                          142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                        Best Local Si
Query Match:
DB:
                                     No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                          Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH9390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                  용
                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                 5 G
                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                     ò
```

```
The present invention describes polymucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (I), (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM0118 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 GTCGGGAGCGCTCCCGCGGCAAGTCTCGGCATCTCCACCGGCGACGAGATCACCGCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 GlyAspVall1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 gegczagecgarecegaregegecekareaagerreceaecerrearararegeceraee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 GCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCGAAGGGCGCACGAGTCCAACGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThralaalaseraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein RA12-P775P-ORF3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 915 BP; 167 A; 280 C; 284 G; 184 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            00
00
00
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ThrLeuAlaGluGlyProProAla 128
8; Page 497-498; 543pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human /M. tuberculosis Ra12 fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-215B-18 (1-128) x AAH93905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
Microbacterium; tuberculosis.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS64141 standard; cDNA; 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.91e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                   the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS64141;
```

WO200173032-A2.

04-OCT-2001

```
the
                                                                                              120
                                                                                                                   322 GGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGTACAGGGAACGTG 381
                                                             321
202 GICGGGAGCGCTCCGGCGAAGICICGGCAICTCCACCGGCGACGIGAICACCGCGGTC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prostate specific protein and its encoding polynucleotide, useful for treatment and diagnosis of prostate cancer.
                             AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                              101 GlyaspvalileServalThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                                     262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC
                                                                                                                                                                                                                                                                                                                                                                                      Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA; prostatic acid phosphatase; PAP; prostate specific membrane antigen; PSMA; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalos MD;
Carter D;
Hural J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skeiky XAW, Hepler WT, Henderson RA, Moneill PD, Houghton RL, Y De BassolsCV, Foy IM;
                                                                                                                                                                                                                                                                                                                                                           Prostate cancer therapy associated cDNA #650.
                                                                                                                                                               121 ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                                                382 ACATTGGCCGAGGGACCCCCGGCC
                                                                                                                                                                                                                                                                멾
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-1999; 99US-0157455P.
04-OCT-2000; 2000US-00679272.
28-MAR-2001; 2001US-00822827.
                                                                                                                                                                                                                                                              ACASS949 standard; cDNA; 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-2001; 2001US-00895793
                                                                                                                                                                                                                                                                                                                              10-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S L
JIANG Y.
FALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-245062/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOY T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HURAL J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-DEC-2002
                                                                                                                                                                                                                                                                                                ACA59949;
                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MCNE/)
(HOUG/)
(DBAS/)
(FOYT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (XUJJ/)
(DILL/)
(MITC/)
(HARL/)
(JIAN/)
(KALO/)
(FANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (STOL/)
(DAYC/)
(VEDV/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CART/)
(LISX/)
(WANG/)
(SKEI/)
(HEPL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HURA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HEND/)
                                                                                                                                                                                                                                                ACA59949
                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                  셤
                                                            셤
                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated prostate-specific polymucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polymucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the polymucleotide and/or poppide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The prostate specific polymucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyGlnAlaMetAlaIleAlaGlyGlnIleLySLeuProThrValHisIleGlyProThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAgpVallleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGCAGGATTCGCCATTCCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 AlaPheLeuGlyLeuGlyValValValAspAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 915 BP; 167 A; 280 C; 284 G; 184 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                              Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       915
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 17; Page 536-537; 579pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-684-215B-18 (1-128) x AAS64141 (1-915)
                                                                                                                                    27-MAR-2000, 2000US-00536857.

09-MAY-2000, 2000US-00568100.

13-JUN-2000, 2000US-00570737.

13-JUN-2000, 2000US-00593793.

27-JUN-2000, 2000US-00565183.

09-AUG-2000, 2000US-00636215.

29-AUG-2000, 2000US-00657279.

06-SEP-2000, 2000US-00657279.

10-OCT-2000, 2000US-00679426.

10-OCT-2000, 2000US-00679426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.91e-58
653.00
100.00%
100.00%
                                                                                                        27-MAR-2001; 2001WO-US009919
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639232/73.
P-PSDB; AAU69902.
                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
```

Alignment Scores:

Score:

21 82

ò g

à 셤 142

dd

```
The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated oDNA. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at directly from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                                                                           82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACGGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAACGGGCATCATCCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGCGTACAGGGAACGTG 381
                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle 20
                                                                                                                                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                           142 GCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCGCAACGGCGCACGACACCGCGTG
                                                                                                                                                                                                                                                                                                                                              GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 groddadgogorcogogdaagrorodgoarcicoacoggogacgroarcacogogo
                                                                                                                                                                                                                                                                                                                                                                                                                           AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                                                                                                                                                                                          Sequence 915 BP; 167 A; 280 C; 284 G; 184 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ral2- P775P-ORF3 construct cDNA sequence SEQ ID NO 834
                                                                                                                                                                     segdata.uspto.gov/sequence.html?DocID=US20020192763
                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                           Indels:
          Example 17; SEQ ID NO 834; 85pp; English
                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                            US-09-684-215B-18 (1-128) x ACA59949 (1-915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL95512 standard; cDNA; 915
                                                                                                                                                                                                                             3.916-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2003
                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL95512;
                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322
                                                                                                                                                                                                                                                                                                                                                                                                                           41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                  Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                                                                                         Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
 ò
                                                                                                                                                                                                                                                                                                                                                      Ωp
                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                            임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New prostate-specific polymucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  915
128
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 G; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 17; SEQ ID NO 834; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 915 BP; 167 A; 280 C;
                                                                                                                                                                                               97US-00806099.
97US-00904804.
98US-00030607.
98US-00115453.
98US-00115453.
99US-00159812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00352616.
99US-00439313.
99US-00443686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-2000; 2000US-00570737.
13-JUN-2000; 2000US-00593793.
27-JUN-2000; 2000US-00605783.
10-AUG-2000; 2000US-00636215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-00483672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-00536857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2000; 2000US-00651236
06-SEP-2000; 2000US-00657279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2000; 2000US-00679426
10-OCT-2000; 2000US-00685166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.91e-58
653.00
100.00%
                                                                                                                                  2001US-00759143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-255649/30.
US200202248-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JAN-2000; 27-MAR-2000; 29-MAY-2000; 212-MAY-2000; 212-MAY-2000; 212-MAY-2000; 213-MAY-2000; 213-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUL-1999;
12-NOV-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                         23-SEP-1998;
15-JAN-1999;
09-APR-1999;
                                                                                                                                  12-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores
                                                                        21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JIAN/)
(KALO/)
(FANG/)
(RETT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HEPL/)
(HEND/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LISX/)
(WANG/)
(SKEI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DILL/)
(MITC/)
(HARL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (STOL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (VEDV/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fanger
Li SX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XU33/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ט
```

```
Example 17; Page 605-606; 691pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB14284 standard; cDNA; 915
                                                                                                             3.91e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003185830-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2003
                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                               322
                                                                                                                                                                                              Н
                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                  382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                ò
ઠે
                                                                                                                                                                                                               g
                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                   ે
                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New prostate-specific proteins and genes, useful in gene therapy, particularly for stimulating an immune response in a patient, or treating prostate cancer in a patient, as well as for diagnosing prostate cancer in a patient.
                                                                                                                                                                                                                                  GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                100
                                                                                                                                                                                                             GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGAACGCGCTTAACGGGCATCATCCC 321
                                                                                                       141
                                                                                                                                                                                                                                              201
                                                                                      40
                                                                                                                         9
                                                                                                                                                           80
                                                                                                                                                                              81
                                                                                                  82 GGGCAGGCGATGGCGGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                                                                                                      GCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCGCAGCAGTCCAACGCGTG
                                                                                                                                                                                               AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                   ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                          AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                      GlyGlnAlaMetAlaileAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson R Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J; Mcneill PD, Houghton RL, Vinals Y De BassolsC, Foy TW, Watanabe Deng T;
                                                                                                                                                                                                                                                                                                                                                                                               therapy; prostate-specific protein; PSP; human;
prostate cancer; 88.
000
                                                                                                                                                                                                                                                                                                                                                                               Prostate tumour specific cDNA sequence SEQ ID 834.
Mismatches:
Indels:
Gaps:
                                  US-09-684-215B-18 (1-128) x ABL95512 (1-915)
                                                                                                                                                                                                                                                                      ThrheuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                         405
                                                                                                                                                                                                                                                                                   382 ACATTGGCCGAGGGACCCCGGGC
                                                                                                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAY-2001; 2001US-00852911.
29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
                                                                                                                                                                                                                                                                                                                           ACC95676 standard; cDNA; 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-2002; 2002WO-US014753
                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-167130/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP
Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; gene
immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200289747-A2
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                               28-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic;
                                                                                                                           41
                                                                                                                                            142
                                                                                                                                                             61
                                                                                                                                                                                202
                                                                                                                                                                                                  81
                                                                                                                                                                                                                  262
                                                                                                                                                                                                                                     101
                                                                                                                                                                                                                                                      322
                                                                                                                                                                                                                                                                      121
Best Local Si
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                      à
                                                                                                      g
                                                                                                                                          å
                                                                                                                                                                              g
                                                                                                                                                                                                 à
                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                     δ
                                                    ò
                                                                    g
                                                                                                                           à
                                                                                                                                                            à
                                                                                        à
```

```
The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; 88; prostate specific cDNA; cytostatic; immunostimulant; gene therapy; cell therapy; vaccine; T-cell epitope; class I major histocompatibility complex allele; MHC; prostate cancer; tumour; antigen presenting cell; gene; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 ACGGCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 droddadcacrocacacaaarcroddarcrocaccacaacararcaccaarc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 eacecectocearcaacroseceacecearescearescearescerraacescarcarca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyAspValileSerValThrTrpGlnThrLy8SerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGCGTACAGGAACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate specific protein P775P-ORF3-RA12 construct cDNA.
                                                                                                                                                                    G; 184 T; 0 U; 0 Other;
                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                            (1-915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                       Sequence 915 BP; 167 A; 280 C; 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACATTGGCCGAGGGACCCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-18 (1-128) x ACC95676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
```

```
Example 17; Page; 101pp; English.
                                                                                                                    06-SEP-2000; 2000US-00657279.
02-OCT-2000; 2000US-00679426.
10-OCT-2000; 2000US-00685166.
09-NOV-2000; 2000US-00709729.
12-JAN-2001; 2001US-00789669.
                                                                                                                                                      09-MAY-2001; 2001US-00852911
29-JUN-2001; 2001US-0085814;
10-DEC-2001; 2001US-00012896
09-MAY-2002; 2002US-00144678
2002US-00294025
                                                                                                                                                                                              Xu J, Stolk JA, Kalos MD;
                                                                                                                                                                                                         WPI; 2003-756193/71.
P-PSDB; ADB14285.
                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                       14-JAN-2000; 2
27-MAR-2000; 2
09-MAY-2000; 2
13-MAY-2000; 2
13-JUN-2000; 2
27-JUN-2000; 2
29-AUG-2000; 2
12-NOV-2002;
                                14-JUL-1998;
23-SEP-1998;
15-JAN-1999;
09-APR-1999;
13-JUL-1999;
12-NOV-1999;
                                                                   18-NOV-1999;
```

```
nucleic acids, antibodies, fusion proteins, T cell populations or antigen presenting cells are used to stimulate an immune response or treat prostate cancer in a patient. The present sequence is a cDNA encoding a fusion protein comprising a prostate specific protein. Note: Except where otherwise indicated, the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030185830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 GGGCAGCAGGCGATCGCGGGCCAGATCAAGCTTCCACCGTTCATATCGGGCCTACC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 gergacercarcrogergacorogenaaccaaaccaagroegococococoracaggaacerg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 AlapheleuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 gecinecresserrissersirares da cares de cares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung tumour protein P801P ORF4 and Ra12 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ung tumour; cancer; T cell; immune response stimulator; cytostatic;
                                                                                                                                                                                                                                                                                                     Sequence 915 BP; 167 A; 280 C; 284 G; 184 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1-915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 ACATTGGCCGAGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215B-18 (1-128) x ADB14284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK39768 standard; cDNA; 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUL-2001; 2001WO-US022058
                                                                                                                                                                                                                                                                                                                                                                                                                      3.91e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MO200204514-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK39768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
        8X88888X8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADB13563 comprising a sequence ADB1487. The peptides comprises a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MMC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific cord. The proteins and peptides, expression vectors, a nest cell transformed with the vector, an isolated antibody (or antigen binding transformed with the vector in a patient (comprising contacting a patient of reagment) that specifically binds to the protein or peptide, detecting the amount of polypeptide or a polypeptide sample with a binding agent that binds to the peptides or a polypeptide cappearing as ADB1358, detecting the amount of polypeptide to a predetermined cutoff value to determine the presence of cancer), a fusion protein coff value to determine the presence of cancer), a fusion protein comprising the peptides or proteins stimulating or expanding T cells specific for a tumour protein comprising contacting T cells with the specific for a tumour protein comprising contacting prostate cancer in a patient and treating prostate cancer in a patient with the peptides or antigen presence of cancer in a patient and treating prostate cancer in a patient with the peptides or antigen presented or an oligonucleotide from that thybridises to nucleic acids encoding them), is used to detect the comprising calls to the patient. The peptides (or an oligonucleotide that hybridises to nucleic acid encoding them), is used to detect the cancer in a patient or appearance of cancer in a patient. The peptides, and encoding them and the peptides or antigen-presenting cells expressing the nucleic acid, are used to cancer in a patient. The peptides is nucleic acids encoding them attimulate or expand I cells specific for a tumour protein. The peptides, are used to detect the antigen-presenting cells the peptides or antigen-presenting cells expressing the nucleic acid, are use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate
                                                                                    97US-00806099.
97US-00904804.
98US-00030607.
98US-00115453.
98US-00115481.
99US-00232149.
99US-00332149.
99US-00332149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-00568100.
2000US-00570737.
2000US-00593793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-00605783.
2000US-00636215.
2000US-00651236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00443686.
2000US-00483672.
2000US-00536857.
```

2000US-00614124. 2000US-00651563. 2000US-00658824.

11-JUL-2000; 29-AUG-2000; 08-SEP-2000;

321

201

80

9

40 81

```
The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a lung cancer in a patient. The polynucleotide is useful for treating a lung cancer in a patient. The polynucleotide is also useful as probe or primer to detect the level of mRNA ancoding a tumour protein. This sequence encodes a lung tumour associated protein or protein. Trament, described in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at they bublished_pot_sequences
                                                                                                                                                                                                                                                                                                                            Novel polynucleotide encoding a lung tumor polypeptide useful for stimulating and/or expanding T cells specific for a tumor protein
                                                                                                                                                                     Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS,
Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                             Example 8; SEQ ID NO.1861; 223pp; English.
26-SEP-2000; 2000US-00671325.
06-OCT-2000; 2000US-00677419.
30-OCT-2000; 2000US-007055.
13-DEC-2000; 200US-00736457.
03-MAY-2001; 2001US-00849626.
                                                                                                                                                                                                                                                               WPI; 2002-164634/21.
P-PSDB; AAU85586.
                                                                                                                               (CORI-) CORIXA CORP.
```

Mcnabb A;

Sequence 945 BP; 150 A; 318 C; 360 G; 117 T; 0 U; 0 Other;

```
yProThr 40
||||||||
GCCTACC 141
                                                                                nArgval 60
||||||||
ACGCGTG 201
                                                                                                                                                                    100
                                                                                                                                   GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC 261
                                                                                                                                                                                       321
                                                                                                                                                                                                                                  381
                                                                                                                          80
20
            CCGATC 81
                                                                                                                                                                                                            GlyAspVallleSerValThrTrpGlnThrLy8SerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                        Alaval
                                                                                                                                                                   AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                  ACATTGGCCGAGGGACCCCGGCC 405
                                                                                                                                                                                                                                                        ThrieuAlaGluGlyProProAla 128
                                                                                                                                                202
                                                                                                                                                                    81
                                                                                                                                                                                                              101
                                                                                                                                                                                                                                  322
                                                                                                                                                                                                                                                        121
```

ਨੋ a Š ద 8

```
Bangur CS, Fanger GR, Wang A, Wang T, Switzer AP, Mcneill PD;
Clapper JD;
                              Human lung cancer protein L801P ORF4/Ral2 fusion protein cDNA.
                                          Human; lung cancer; ss; lung tumour; cytostatic; vaccine;
T cell expansion; CD4; CD8; RA12; gene.
ACA12097 standard; cDNA; 945 BP.
                                                                                                           13-DEC-2000; 2000US-00736457.
                                                                                                 03-MAY-2001; 2001US-00849626
                    (first entry)
                                                                                                                                           SWITZER A P. MCNEILL P D. CLAPPER J D.
                                                                                                                                                                                  WPI; 2003-352750/33.
P-PSDB; ABU69561.
                                                                                                                      BANGUR C S.
FANGER G R.
WANG A.
                                                                           US2002197669-A1.
                                                           Homo sapiens.
Synthetic.
                    06-JUN-2003
                                                                                      26-DEC-2002
          ACA12097;
                                                                                                                      (BANG/)
(FANG/)
(WANG/)
                                                                                                                                      (WANG/)
(SWIT/)
(MCNE/)
                                                                                                                                                        (CLAP/)
```

Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer.

Example 8; Page; 72pp; English.

The invention relates to a polymucleotide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in the specification, or a sequence (S2) mentioned in specification, or a sequence consisting of at least 20 contiguous residues complement of S1, sequences consisting of at least 20 contiguous residues of S1, sequences that hybridise to S1, sequences having 75%, preferably complement by Lo S1, or degenerate variaties of S1. Also included are an isolated polypeptide (comprising a sequence sequence from any one of the 4 amino acid sequences mentioned in the specification, a sequence concoded by the polymucleotide, or sequences having at least 70%, comprising the polymucleotide operably linked to an expression vector comprising the polymucleotide operably linked to an expression vector comprising the polymucleotide operably linked to an compression control sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that expression controls expending the presence of a cancer of a protein (comprising contacting) collises to S1 under moderately stringent conditions, stimulating and/or expanding T cells specific for a tumour or antigen presenting cells, under conditions and for a time sufficient to permit the stimulation and/or expanding T cells specific for a tumour contaction presenting cells, under conditions and for a time sufficient collisated from a patient (by incubating CD4 + and/or CD8 cells isolated from a patient with the polymucleotide, protein or presenting cells, under express the polymucleotide, protein or composition and thus inhibiting the development of a cancer in a patient with the polymucleotide, protein or stimulating and immune response in a patient (patient (patient, and thus inhibiting the development of a cancer in a patient (patient express the polymucleotide, protein or antigence of a cancer in a patient (patient express). The composition for stimulating and immune response in a patient (

```
patient. The protein and oligonucleotides are useful in pharmaceutical compositions, e.g. vaccines. The polymucleotide is also useful as a probe or primer for nucleic acid hybridisation, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polymeptides and proteins in tumour cells. An amplified portion of the polymeptides and proteins in tumour cells. An amplified portion of the polymoleotide is useful for isolating a full-length gene from a suitable library. The present sequence encodes a fusion protein of human RAL2 with the protein product of a cDNA (full length, extended or partial) isolated from a library derived from lung tumour/cancer cells. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at sequence.html?DocId=20020197669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141
                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                         40
                                                                                                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                          GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                          GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyAspVall1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                                                                                                                       ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlalleProIle
                                                                                                                                                                                                                                                                                                                                             ACGCCCCCCCCATCCCACTCCCACCTCCCAGGCTGGGCAGGGATTCCCCATTCCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                           GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ġ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; vaccine; gene therapy; cancer; gene;
                                                                                                                                                                    Sequence 945 BP; 150 A; 318 C; 360 G; 117 T; 0 U; 0 Other;
                                                                                                                                                                                                         cancer therapyand diagnosis associated DNA #4
                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                 (1-945)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACATTGGCCGAGGGACCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrienAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                 US-09-684-215B-18 (1-128) x ACA12097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUL-2001; 2001US-00902941
                                                                                                                                                                                                         4.06e-58
653.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA; 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002172952-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAY-2003
                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACA03283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACA03283;
                                                                                                                                                                                                                                                                                                                        н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322
                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                             41
                                                                                                                                                                                                                                                                                                                                                                                                                                                     142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                        Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lung
                                                                                                                                                                                                           ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
  8888888888888888
                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                           8 6
                                                                                                                                                                                                                                                                                                                                                                                                                   8 6 6 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \ddot{o}
                                                                                                                                                                                                                                                                                                                        8
```

```
The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polynucleotide associated with the compositions and methods for the therapy and diagnosis of lung cancer.
                                                                                                                                                                                                                                                                                                                                                       or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyapvalileServalThrTrpGlnThrLyaSerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 ACGGCCGCGTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGAATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAslaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 GCCTTCCTCGGCTTGGGTGTTGTCGACACAACGGCAACGCGCACGAGGTCCAACGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 GACGGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAACGGGCATCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                     New polynucleotide, useful for preparing a composition for treating inhibiting development of cancer, e.g. lung cancer.
                                                                                                                                                                                                                                                                                                Mcnabb
                                                                                                                                                                                                                                                                                    ž.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 945 BP; 150 A; 318 C; 360 G; 117 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                  , Watanabe Y, Johnson JC, Retter P
Fanger GR, Vedvick TS, Bangur CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 640000
440
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                Example 8; SEQID NO 1861; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-684-215B-18 (1-128) x ACA03283 (1-945)
30-UUN-1999; 99US-00346492.
15-OCT-1999; 99US-00419356.
17-DEC-1999; 99US-00466867.
30-DEC-1999; 99US-004766867.
30-DEC-1999; 99US-004766867.
22-MAR-2000; 2000US-00519642.
22-MAR-2000; 2000US-00546259.
27-APR-2000; 2000US-005614124.
29-AUG-2000; 2000US-00614124.
29-AUG-2000; 2000US-00611325.
26-SEP-2000; 2000US-00671325.
26-SEP-2000; 2000US-00671325.
30-OCT-2000; 2000US-00671325.
313-DEC-2000; 2000US-007705765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.06e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                  Wang T,
Carter D, Fa
                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                           WPI; 2003-328427/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                  Henderson RA,
Durham M, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   જે
```

80

381

201

141

81 40

186 9 306

80

426

121

셤

01-MAY-2002

ABL49256;

Homo sapiens

3-JAN-2002.

ABLA9256
ID COLL
ID ABLA9256
ID COLL
I

us-09-684-215b-18.rng

```
The present invention describes isolated human lung carcinoma polymucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a center in a patient, by obtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polymucleotide that hybridises to the oligonucleotide and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer.
                                                                                                                                                                                                          GlyAspVall1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
Moneill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
                  247 GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC
                                                                                                                                                                                                                                                                                                     41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                            61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
GlyGlnalaMetAlaIleAlaGlyGlnIleLySLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human lung cancer associated DNA sequence SEQ ID NO:351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Page 339-340; 381pp; English.
                                                                                                                                                                                                                                                                                                                                                         ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                           450
                                                                                                                                                                                                                                                                                                                                                                             AB092442 standard; DNA; 1012 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-DEC-2000; 2000US-00735705.
07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-2001; 2001WO-US047576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-583465/62.
P-PSDB; ABP61919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200247534-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                             427
                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ92442;
                                                                                                                                                                                                                                                                                      101
     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                8 8
     8 6 8 6
                                                                                                                                    $ A
                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                           8 8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes human lung tunnour proteins. Human lung tunnour proteins and polynucleotides have eytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tunnour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tunnour proteins are useful for treating lung cancer or stimulating an immune response. ABL48559 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                  Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine; immune response; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response.
                                                                                                                                                                                                                Ral2/N-terminal portion of L763P fusion polynucleotide SEQ ID NO:351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang T, Wang A, Skeiky YAW, Li SK, Kalos MD, Henderson RA, Moneill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR, Vedvick TS, Carter D, Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; 289 G; 199 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1012
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-684-215B-18 (1-128) x ABL49256 (1-1012)
       ThrieuAlaGluGlyProProAla 128
                          382 ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 332; 374pp; English.
                                                                                                               ABL49256 standard; cDNA; 1012 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUN-2000; 2000US-00606421.
02-A/G-2000; 2000US-00639940.
21-A/G-2000; 2000US-0064597.
15-SEP-2000; 2000US-00662786.
09-607-2000; 2000US-00685656.
12-DEC-2000; 2000US-00735705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1012 BP; 235 A; 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.416-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUN-2001; 2001WO-US021065
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-090513/12.
P-PSDB; ABB74999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                               WO200200174-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
```

nvention

ઠે g us-09-684-215b-18.rng

```
GlyAspvallleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                  127 GGCCAGGCGATGGCGATCGCGGGCCAGAGCTTCCCACGTTCATATCGGGCCTACC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                           306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC 366
                                                                                                                                                                                                                                                                           ACGCCCCCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC 126
                                                                                                                                                                                                                                                                                                                                                                                        amount of polynucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABQ22486 and ABP61866 to ABP61992 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                  60
                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCGGGAGCGCTCCGGCGGCAAGTCTCCGCATCTCCACCGGCGACGTGATCACCGCGGTC
                                                                                                                                                                                                                                                                                                               GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                   ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                              ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle
                                                                                                     Sequence 1012 BP; 235 A; 289 C; 289 G; 199 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein L763P N-terminal/Ra12 fusion DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; lung cancer; gene therapy; vaccine; human; lung squamous cell carcinoma; gene; ss; ral2.
                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                     (1-1012)
                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                     US-09-684-215B-18 (1-128) x ABQ92442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00040802.
98US-00123912.
98US-00221107.
99US-00285479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA28441 standard; cDNA; 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-00007700
                                                                                                                                             4.41e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2003064947-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAR-1998;
27-JUL-1998;
22-DEC-1998;
02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour
                                                                                                                                 gnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-2003
                                                                               invention
                                                                                                                                                                                                                                                                                                                                                                                                                                            247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427
                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                  41
                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA28441;
                                                                                                                                                                                                                                                               Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                 Best Local Si
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                               ⋩
                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                              \dot{\delta}
                                                                                                                                                                                                                                                                                                                                                                                                                                       ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
    88888888888
```

```
The invention describes isolated polynuclectides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer. A new isolated polynuclectide comprises: any of the 22 fully defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above; at sequence that hybridise to any of the nucleotide sequences cited above; a sequence that hybridise to any of the nucleotide sequences under highly stringent conditions; a sequence that is at least 75 or 90% identical the above nucleotide sequences; or degenerate variants of the above the above nucleotide sequences. The composition and methods are useful in nucleotide sequences. The stringent cancer, particularly lung cancer, in gene therapy and in vaccines. This sequence encodes a fusion protein of human lung tumour protein L673P N-terminal and Ral2.
                                                                                                                                                                                                                                                                                                Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
Mcneill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1012 BP; 235 A; 289 C; 289 G; 199 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1012
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1-1012)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 251-252; 296pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-18 (1-128) x ADA28441
        10-DEC-1999; 9903-0046696.
10-JAN-2000; 2000US-0048684.
22-FEB-2000; 2000US-00510376.
04-AFB-2000; 2000US-0054615.
28-JUN-2000; 2000US-0066421.
28-JUN-2000; 2000US-00669421.
15-SEP-2000; 2000US-0066596.
15-SEP-2000; 2000US-0068696.
15-MAY-2001; 2000US-0068696.
17-DEC-2000; 2000US-0068696.
17-DEC-2000; 2000US-0068696.
17-DEC-2000; 2000US-0068696.
17-DEC-2000; 2000US-0068696.
28-JUN-2001; 2001US-00857778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.416-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-540798/51.
                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ADA28441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
ઠે
```

366

AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisBro 100

81 307

8 8

ď

247 GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGGTC 306

ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal

187 61

127 geschescearescearcecescearcaascricceaccarcarrararescerace 41 AlapheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal

21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr

186

9

40

246

80

67 ácedecedecentedanadentecedecededededededededadanicedanicedane 126

g

ò 셤 ઠે 셤 à

80

183

9

363

15-JUL-2002

ABK69714

427 121

ð 셤

g

RESULT 26 ABK69714

101 367 gene; ss.

Human;

11-APR-2002.

```
The present invention describes compounds (1) for the immunotherapy and diagnosis of colon cancer. Also described: (1) a method for detecting the presence of cancer in a patient; (2) a method for stimulating and/or expanding T cells specific for a tumour protein; (3) an isolated T cell population comprising T cells prepared by the method of (2); (4) a method for stimulating an immune response in a patient; (5) a method for tradical cancer in a patient; and (6) a method for inhibiting the development of cancer in a patient. (1) have immunostimulant and evelopment of cancer in a patient. (1) have immunostimulant and and Apps3543 to Apps351 represent human colon cancer/tumour related sequences used in the exemplification of the present invention
                                                                                                                                                                                        244 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGATGACGGGCTTAACGGGGATCATCCC 303
                                                                                                                                                                                                                                   GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR, Meagher MJ, Stolk JA;
3, Wang A, Clapper JD, Skeiky YAW;
64 GGGCAGGCGATGGCGATCGCGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 123
                                                                                                                     81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                         61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                  AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValAlaPyal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ancer, colon tumour, immunotherapy, diagnosis, cancer, response, immunostimulant, cytostatic, vaccine, gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide, useful for the preparation of a composition for stimulating an immune response against, or treating, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human colon tumour cDNA for Ral2-C884P-PCRX2 SEQ ID NO:1084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lodes MJ, Secrist H, Benson DR,
Jiang Y, Smith CL, King GE,
GR, Vedvick TS, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 474-475; 537pp; English.
                                                                                                                                                                                                                                                                                                        121 ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                          387
                                                                                                                                                                                                                                                                                                                             364 ACATTGGCCGAGGGACCCCCGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                             ABZ33699 standard; cDNA; 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-2001; 2001US-00833263.
03-AUG-2001; 2001US-00922217.
19-DEC-2001; 2001US-00025380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-2002; 2002WO-US011475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-067548/06.
P-PSDB; ABPS5373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; colon ca
tumour; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200283070-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang I, Jia
Fanger GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ33699;
                                                                                                                                                                                                                                         101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu J,
Wang T
                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                 원
                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                              용
                                                                                                                                                                      ð
                                                                                                                                                                                                                                          8
                            8
                                                           원
                                                                                                 ઠ
                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated WTI polynucleotide (I) and polypeptide encoded by (I). The WTI polynucleotides and polypeptides are used for treating and detecting cancer in a patient, and for stimulating an immune response in patient ABK69648-ABK69724 represent WTI coding sequences and PCR primers of the invention
                       GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                             GGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCACGCGTACAGGGAACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                               mouse; cytostatic; immunostimulant; WT1; cancer; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for treating and diagnosing cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smithgall M, Moulton G, Vedvick TS;
Evans L, Spies AG, Boydston J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 A; 355 C; 291 G; 172 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1035
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-09-684-215B-18 (1-128) x ABK69714 (1-1035)
                                                                                        ThrieuAlaGluGlyProProAla 128
                                                                                                                          ACATTGGCCGAGGGACCCCCCGGCC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 240; 260pp; English.
                                                                                                                                                                                             BP
                                                                                                                                                                                             ABK69714 standard; cDNA; 1035
                                                                                                                                                                                                                                                                                               human Ra12/WT1-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-OCT-2000; 2000US-00684361.
09-OCT-2000; 2000US-00685830.
15-FEB-2001; 2001US-00938864.
24-AUG-2001; 2001US-00938864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.53e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2001; 2001WO-US031139
                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mcneill PD,
Mossman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-352217/38.
P-PSDB; ABG33391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP. (GAIG/) GAIGER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВР;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200228414-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1035
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                 DNA encoding
```

Gaiger A, N Sleath PR,

Best Local S Query Match:

ઠે 원

```
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                               GGGCAGGCGATGGCGGGGCCAGCTCCACCGTTCATATCGGGCCTACC 141
                                                                                                                                                                                                                       gradegadedecrecededaagreredecarerecadedecadedaareacededere 261
                                                                                                                                                                                                                                       AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                        GACGGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC 321
                                                                                                                                                                                                                                                                        GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                    GCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCGACGAGTCCAACGCGTG 201
                                                                                                                                                                      9
                                                                                                                                                                                                     80
                                                                                                   20
                                                                                                                                   40
                                                                                                                  ACGCCCCCCCCTCCCATAACTTCCCAGCTCCCCAGGGTGGGCCAGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                             Human, Wilm's tumour antigen; WT1; cytostatic; antigen, T cell; antigen-presenting cell; CD4+; CD8+; immune response; cancer; vaccine;
                                                                                                                                                                                                      ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                   ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                   GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                      AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
274 G; 262 T; 0 U; 0 Other;
                        1103
1128
0000
0000
                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                  US-09-684-215B-18 (1-128) x ABZ33699 (1-1035)
                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                           405
                                                                                                                                                                                                                                                                                                          ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                             Human RA12/WT1 E fusion protein cDNA.
                                                                                                                                                                                                                                                                                                                         ACATTGGCCGAGGACCCCCGGCC
252 A; 247 C;
                                                                                                                                                                                                                                                                                                                                                            ADB67590 standard; cDNA; 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1998; 98US-00164223.
25-MAR-1999; 99US-00276484.
06-OCT-2000; 2000US-00684361.
09-OCT-2000; 2000US-00685830.
                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen-presenting cell; CD4+
leukaemia; antigen; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-FEB-2001; 2001US-00785019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-2001; 2001US-00938864
                      4.53e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAIGER A.
MCNEILL P D.
SMITHGALL M.
BP;
                                                 Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2003072767-A1.
                                         Percent Similarity:
Sequence 1035
                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-2003
                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-APR-2003
                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                             ADB67590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GAIG/) (MCNE/) R
                                                                                                   Н
                                                                                                                                    21
                                                                                                                                                                      41
                                                                                                                                                                                      142
                                                                                                                                                                                                      61
                                                                                                                                                                                                                        202
                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                        262
                                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                          322
                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                          382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric
                                                         Query Match:
DB:
                                                 Best Local
                          RESULT 2
ADB67590
                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                         음
                                                                                                                                                                                                                                                                                                                         음
                                                                                                                  g
                                                                                                                                                  d
                                                                                                                                                                     8
                                                                                                                                                                                  g
                                                                                                                                                                                                 8
                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                          ð
                                                                                                  ò
                                                                                                                                    à
```

```
The invention relates to an isolated Wilm tumour (WTI) polymucleotide comprising a full length protein, truncated protein, mutated protein or fusion protein. Also included are the encoded WTI proteins, expression vectors, host cells, antibodies, detecting the presence of a cancer in a partient by contacting a biological sample with a binding agent that binds to a WTI protein, an oligomucleotide that hybridises to a WTI compression or antigen. Presenting T cells with the WTI polymucleotide, the WTI protein or antigen. Presenting T cells with the WTI polymucleotide, the WTI protein, and a second component selected from the WTI polymucleotide, the WTI protein, inhibiting the CC composition (CI) (comprising physiologically acceptable carriers and composition (CI) (comprising physiologically acceptable carriers and composition calls that express the WTI protein, inhibiting the CC development of a cancer in a patient (by incubating CD4+ and/or CD8+ T cells isolated from a patient with the WTI polymucleotide, the WTI protein, inhibiting the CC development of a cancer in a patient (by incubating CD4+ and/or CD8+ T cells isolated from a patient with the WTI polymucleotide, the WTI cells isolated from a furger presenting cells that express the WTI polymucleotide, the WTI cells isolated from a furgen presenting cells that express the WTI polymucleotide, the WTI cells for the patient (CZ) (comprising a WTI polympetide resuspended in a composition (CZ) (comprising a wTI polympetide resuspended in a composition (CZ) (comprising a wTI polympetide resuspended in a patient of an immunogenic portion of WTI polympetides or and MFP-SE or Enhanzyn). Also disclosed as anew are polympetides or protein are useful for stimulating immune response in a patient, and patient, for writing and treating metastatic diseases cancer. CI is useful for inhibiting the development of a malignant composition as mapple. Ab (binding agent for the WTI protein is useful semple and protein are conventing and treating metastatic for determining a fundar co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGGCAGGGATTCGCCATTCCGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel Wilms tumor polynucleotides encoding WT1 polypeptides, useful f
detecting the presence of cancer in a patient, and in pharmaceutical
compositions, e.g. vaccines, for treating cancers e.g. leukemia.
                                                                                                                                                                                                                                                                      Smithgall M, Moulton G, Vedvick TS;
Evans L, Spies AG, Boydston J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1035 BP; 217 A; 355 C; 291 G; 172 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-684-215B-18 (1-128) x ADB67590 (1-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detecting the presence of cancer in
encodes a Human WT1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 145; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    653.00
100.00$
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.53e-58
                                                                                                                                                                                                                                                                      Mcneill PD,
Mossman S,
MOULTON G.
VEDVICK T S.
SLEATH P R.
                                s,
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-605957/57.
                                                                                              MOSSMAN S.
EVANS L.
SPIES A G.
                                                                                                                                                                                                        BOYDSTON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ADB67593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                          Gaiger A, 1
Sleath PR,
                                                                 (SLEA/)
(MOSS/)
(EVAN/)
(SPIE/)
(BOYD/)
```

ð

8 & 8

à q à

```
GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGGCATCATCCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 gereacercarcrosereaccrescaaaccaastcsasercesececaceceracassas
cells from a biological sample. The polynucleotide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This sequence encodes a lung tumour associated protein or protein fragment, described in the method of the invention. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 GCCTTCCTCGGCTTGGGTGTTGTCGACAACGCCAACGGCGCACGAGTCCAACGGGTG
                                                                                                                                                                                                                                                                                                                                                                                       ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                        22 Acceccecercearaacriccaecrerceassessessessessesriceccaricceare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 erceseagecerreceseaseacrasereresearerecaceseseacereareacesesere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 ASPGIVALAPPROILEASDSERALATARLAMETALAASPALALEUASDGIVHISHISPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                       Sequence 1155 BP; 239 A; 346 C; 302 G; 268 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; lung cancer; ss; lung tumour; cytostatic; vaccine;
T cell expansion; CD4; CD8; RA12; gene.
                                                                                                                                                                                                              1155
128
0
0
0
0
                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                US-09-684-215B-18 (1-128) x ABK39775 (1-1155)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Ral2-L985P fusion protein cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACATTGGCCGAGGGACCCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACA12104 standard; cDNA; 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-2000; 2000US-00736457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-2001; 2001US-00849626
                                                                                                                                                                                                            5.17e-58
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BANG/) BANGUR C S.
                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002197669-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
                                                                                                                                                                                             Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACA12104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Нопо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACA12104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8888888888
                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           쉱
                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for treating a
                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                       GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                363
                                                                                               183
                                                                                                                                                                         243
                                                                                                                                    80
                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۷
                                                                                                                                                                                                                                    GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGGCATCATCCC
                                                                                                                                                                                                                                                                                                                GGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGCGCACGCGTACAGGAACGTG
  GGGCAGGCGATGGCGATGGGCGAGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                       AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                         Gredesaccerecececasarerececarerececaceaccasecarereaccecere
                                                                                                                                                                                                                AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcnabb
                                                                                               GCCTTCCTCGGCTTGGGGTGTTGTCGACAACGGCAACGCCGCACGCGACGCGTG
                                                                                                                                    ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour; cancer; T cell; immune response stimulator; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotide encoding a lung tumor polypeptide useful for
stimulating and/or expanding T cells specific for a tumor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe Y, Henderson RA, Johnson JC, Retter MW; is M, Carter D, Fanger GR, Vedvick TS, Bangur CS, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 1875; 223pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding Ral2-L985P fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                         387
                                                                                                                                                                                                                                                                                                                                                                     ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                         ACATTGGCCGAGGGACCCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2000) 2000US-00651563.

08-SEP-2000) 2000US-00658824.

26-SEP-2000) 2000US-00671325.

06-OCT-2000) 2000US-0077419.

30-OCT-2000) 2000US-00702705.

13-DEC-2000) 2000US-00745457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK39775 standard; cDNA; 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US022058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-00614124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang T, Watanabe Y, Hen
Marnerakis M, Carter D,
Wang A, Fanger N, Switz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-164634/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAU85593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200204514-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                         364
                                                         41
                                                                                               124
                                                                                                                                                                         184
                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                    244
                                                                                                                                                                                                                                                                                         101
                                                                                                                                                                                                                                                                                                                              304
                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK39775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene; ss
                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lung
```

261 100

80

141

40

81

201

9

```
Wang A, Wang T, Switzer AP, Mcneill PD;
                                                                         Fanger GR,
                              SWITZER A P. MCNEILL P D. CLAPPER J D.
FANGER G R.
            WANG A.
                      WANG
                                                                         Bangur CS,
                               (SWIT/) S
(MCNE/) N
(CLAP/) (
 (FANG/)
                      WANG/
```

Clapper JD;

WPI; 2003-352750/33. P-PSDB; ABU69568.

Novel lung cancer polymucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer.

Example 10; Page; 72pp; English.

The invention relates to a polynucleotide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in the specification, or a sequence (S2) mentioned in specification, complement of S1, sequences consisting of at least 20 contiguous residues of S1, sequences that hybridise to S1, sequences having 75*, preferably 90*, identity to S1, or degenerate variants of S1. Also included are an isolated polympetide (comprising a sequence (S3) selected from any one of the 4 amino acid sequences mentioned in the specification, a sequence encoded by the polymucleotide, or sequence having at least 70*, preferably 90*, identity to a sequence encoded by the polymucleotide, and expression overcor comprising the polymucleotide operably linked to an expression control sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that expression control sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that conditions, stimulating and/or expanding T cells specific for a tumour protein comprising or the polympetide, detecting the presence of a cancer of antigen-presenting cells, under conditions and for a time sufficient or antigen-presenting cells, under conditions and for a time sufficient conditions, stimulating and/or expanding T cells specific for a time sufficient content of a cancer in a patient (by incubating CD4* and/or CD8*, T cells isolated from a patient (by incubating CD4* and/or CD8*, T cells isolated from a patient with the polymucleotide, protein or antigen presenting cells, and thus inhibiting the development of a cancer in a patient (particularly lung cancer in a patient (patient) and inmune response in a patient of patient and protein and oligomolectid polypeptides and proteins in tumour cells. An amplified portion of the polymuclectide is useful for isolating a full-length gene from a suttable library. The present sequence encodes a fusion protein of human RA12 with the protein product of a cDNA (full length, extended or partial) isolated from a library derived from lung tumour/cancer cells. Note: The sequence from a library derived from lung tumour/cancer cells. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from tl segdata.uspto.gov/sequence.html?DocId=20020197669

BP; 239 A; 346 C; 302 G; 268 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: 653.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match:

JS-09-684-215B-18 (1-128) x ACA12104 (1-1155)

1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlyPheAla11eProlle 20	22 AcGeccacatraactrccaactacccaaaaactrccaaaaacaaaaaaaa	21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40	82 GGGCAGGCGATGGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 141	41 AlaPheLeuGlyUeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60	142 GCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCGACGGCGCACGAGTCCAACGGCGTG 201	61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80	202 GICGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC 261	81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100	262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAACGGGCATCATCCC 321	101 GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120	322 GGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGCACGCGTACAGGGAACGTG 381	121 ThrLeuAlaGluGlyProProAla 128	382 ACATTGGCCGAGGACCCCCGGCC 405
8	업	à	QO	ò	qq	ò	q	ò	q	ò	q	ò	q _Q

Search completed: April 29, 2004, 23:03:11 Job time : 368.096 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

```
April 29, 2004, 20:32:52; Search time 3670.05 Seconds (without alignments) 1511.672 Million cell updates/sec
                                                                                                                                                                                                          US-09-684-215B-18
653
1 TAASDNFQLSQGGQGFAIPI......ÇTKSGGTRTGNVTLABGPPA 128
nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3470272 segs, 21671516995 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                    7.00.5
                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Xgapop 10.0, Xgapext (
Ygapop 10.0, Ygapext (
Fgapop 6.0, Fgapext Delop 6.0, Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenEmbl:*

1: gp ba:*

4: gb htg:*

5: gb htg:*

6: gb om:*

7: gb pa:*

10: gb om:*

10: gb om:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                          Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number
   OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                             е
С
                                                                         Run
```

e	: em_htg hum:*	em htg	em_bt	em ht	: em_ht	em ht	: em_ht		: em sy	em ht	em htgo	em htgo
29:	30:	31:	32:	33:	34:	35:	36:	37:	38:	39:	40:	47:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

tch Length DB ID 0.0 675 6 AR400535 0.0 675 6 AR400535 0.0 675 6 AR400532 0.0 675 6 AR400549 0.0 675 6 AR400549 0.0 675 6 AR400549 0.0 675 6 AR400549 0.0 822 6 AR360952 0.0 824 6 AR360952 0.0 824 6 AR360952 0.0 900 6 AR36090 0.0 915 6 AR36090 0.0 1012 6 AR36099 0.0 1012 6 AR36099 0.0 1155 6 AR36099 0.0 1164 6 AR36099 0.0 1164 6 AR36099 0.0 1203 6 AR36099 0.0 1203 6 AR36099 0.0 1203 6 AR36099 0.0 1155 6 AR36099 0.0 1164 6 AR36099 0.0 1164 6 AR36099 0.0 1165 6 AR36099 0.0 1578 6 AR36099 0.0 1578 6 AR36099 0.0 1578 6 AR320099 0.0 1752 6 AR320099 0.0 1752 6 AR320099 0.0 1752 6 AR320099 0.0 1752 6 AR320099 0.0 1758 6 AR320			•			SUMMARIES		
1 653 100.0 675 6 AR405835 AR40053 3 653 100.0 675 6 AR405802 AR40580 4 653 100.0 675 6 AR201049 AR20104 5 3 100.0 675 6 AR201049 AR20104 6 653 100.0 675 6 AR201049 AR20104 8 653 100.0 822 6 AR201044 AR20104 9 653 100.0 900 6 AR201054 AR20105 10 653 100.0 900 6 AR201061 AR201061 11 653 100.0 915 6 AR201061 AR201061 12 653 100.0 915 6 AR201061 AR201061 14 653 100.0 915 6 AR201069 AR201061 15 67 100.0 915 6 AR201069 AR201061 16 633 100.0 915 6 AR201069 AR20107	Result No.	Ŭ O	% Query Match	Length	DB		escript	ion
653 100.0 675 6 AR400535 AR40053 653 100.0 675 6 AR400535 AR405802 AR405802 653 100.0 675 6 AR267648 AR267648 AR267649 653 100.0 822 6 AR277645 AR351489 AR351489 653 100.0 822 6 AR251590 AR351489 AR351489 653 100.0 900 6 AR251281 AR351489 AR351489 653 100.0 915 6 AR261281 AR351489 AR351489 653 100.0 915 6 AR261281 AR361281 AR361281 653 100.0 915 6 AR261281 AR361289 AR361289 653 100.0 915 6 AR261281 AR361289 AR361289 653 100.0 915 6 AR26189 AR361289 AR361289 653 100.0 915 6 AR26189 AR36189 AR36189 653 100.0 915 6 AR261816	1	1 29	0.00	675	•	26127	61272	UJ
653 100.0 675 6 AR405802 AR405802 AR405802 653 100.0 675 6 AX201049 AX201049 AX201049 653 100.0 675 6 AX201049 AX201049 AX201040 653 100.0 675 6 AX301499 AX201049 AX201040 653 100.0 900 6 AX301499 AX301149 AX201041 653 100.0 900 6 AX301499 AX301149 AX301149 653 100.0 900 6 AX301699 AX301149 AX301149 653 100.0 915 6 AX201044 AX301144 AX301149 653 100.0 915 6 AX201044 AX301144 AX301144 653 100.0 915	7		ö.	67		0053	n	
653 100.0 675 6 AX201049 AX20104 653 100.0 822 6 AX369152 AX36150 653 100.0 822 6 AX369152 AX36190 653 100.0 894 6 AX369152 AX36190 653 100.0 900 6 AX369152 AX31690 653 100.0 915 6 AX405811 AX40591 653 100.0 915 6 AX201061 AX26106 653 100.0 915 6 AX201061 AX26106 653 100.0 915 6 AX201061 AX201061 653 100.0 915 6 AX201061 AX201061 653 100.0 915 6 AX369151 AX201061 653 100.0 1012 6 AX369151 AX201061 653 100.0 1012 6 AX369156 653 100.0 1012 6 AX369165 653 100.0 1203 6 AX369165 653 100.0 1557 6 AX361955 653 100.0 1557 6 AX361955 653 100.0 1578 6 AX361939 653 100.0 1578 6 AX361936 653 100.0 1752 6 AX361939 653 100.0 1752 6 AX361939 653 100.0 1752 6 AX361959 653 100.0 1752 6 AX316986 653 100.0 1752 6 AX316986 653 100.0 1752 6 AX316989 653 100.0 1752 6 AX3161959 653 100.0 1752 6 A	М		ë.	67		2580	0	V2 '
653 100.0 675 6 AX267848 AX26784 653 100.0 822 6 AX369152 AX35148 653 100.0 822 6 AX369152 AX35148 653 100.0 822 6 AX369162 AX36596 653 100.0 900 6 AX365960 AX26768 653 100.0 915 6 AX26181 AX26128 653 100.0 915 6 AX26161 AX26786 653 100.0 915 6 AX26161 AX26786 653 100.0 915 6 AX267860 AX26786 653 100.0 915 6 AX267860 AX26786 653 100.0 1012 6 AX369151 AX36916 653 100.0 1012 6 AX369165 AX26786 653 100.0 1012 6 AX369165 AX36918 653 100.0 1203 6 AX369165 AX46982 653 100.0 1203 6 AX26787 653 100.0 1464 6 AX369165 AX46982 653 100.0 1464 6 AX369186 AX36918 653 100.0 1464 6 AX369196 AX36918 653 100.0 1464 6 AX361955 AX46982 653 100.0 1464 6 AX361955 AX46982 653 100.0 1464 6 AX361955 AX46982 653 100.0 1557 6 AX36195 AX36195 653 100.0 1557 6 AX36195 AX36195 653 100.0 1578 6 AX36195 AX36195 AX36198 653 100.0 1578 6 AX36199 AX36195 AX36196 653 100.0 1578 6 AX36199 AX36196 AX15619 653 100.0 1578 6 AX36199 AX36196 AX36196 653 100.0 1752 6 AX36199 AX36196 AX36196 653 100.0 1752 6 AX36199 AX36196	4		ġ	67		0104	4	· .
653 100.0 822 6 AX351495 653 100.0 822 6 AX351489 653 100.0 824 6 AX351489 653 100.0 824 6 AX351489 653 100.0 900 6 AX355960 653 100.0 915 6 AX256261 653 100.0 915 6 AX256281 653 100.0 915 6 AX201061 653 100.0 1012 6 AX369151 653 100.0 1125 6 AX369154 653 100.0 1125 6 AX369165 653 100.0 11203 6 AX201078 653 100.0 1203 6 AX320208 653 100.0 1557 6 AX322016 653 100.0 1557 6 AX322016 653 100.0 1557 6 AX322016 653 100.0 1578 6 AX322016 653 100.0 1578 6 AX322038 653 100.0 1578 6 AX322031 653 100.0 1758 6 AX322031 653 1	2		0	67		5784	4.	"
653 100.0 822 6 AX359152 AX35915 653 100.0 900 6 AR220690 AX35596 653 100.0 915 6 AR40541 AR40544 653 100.0 915 6 AR40541 AR40581 653 100.0 915 6 AR405811 AR22069 653 100.0 915 6 AR201661 AR227764 653 100.0 915 6 AR20764 AX367764 653 100.0 915 6 AX369151 AX26796 653 100.0 1012 6 AX369151 AX26796 653 100.0 1012 6 AX369156 653 100.0 1012 6 AX369165 653 100.0 1203 6 AR405823 AX369165 653 100.0 1203 6 AR405823 AX369165 653 100.0 1203 6 AR405823 AX369165 653 100.0 1203 6 AR229410 AX26796 653 100.0 1464 6 AR3292028 AX369165 653 100.0 1464 6 AR3292028 AX369166 653 100.0 1557 6 AX361955 AX36193 653 100.0 1557 6 AX361939 AX36193 653 100.0 1578 6 AX361939 AX36193 653 100.0 1578 6 AX361936 AX361936 AX36193 653 100.0 1578 6 AX361936 AX361936 AX361936 653 100.0 1752 6 AX361939 AX361936 AX361936 653 100.0 1752 6 AX361959 AX361936 AX361936 653 100.0 1752 6 AX361959 AX361936 A	9		ö.	85		7764	41	٠, ،
653 100.0 894 6 AX351489 AX35596 653 100.0 900 6 AX365960 AX365960 AX365960 653 100.0 915 6 AX405811 AX405811 AX405811 AX405811 AX50100 915 6 AX201061 AX501061 AX501061 AX50106 AX365960 AX365990 AX365960 AX365960 AX365960 AX365960 AX365960 AX365960 AX365990 AX365960 AX3659	7		0	85		5915	n o	
653 100.0 900 6 AR220690 AX3650690 AX3650690 6 53 100.0 915 6 AR261281 AX400544 AX40544 AX40544 653 100.0 915 6 AX405811 AX20106 653 100.0 915 6 AX267860 AX365060 AX365060 653 100.0 915 6 AX267860 AX267860 AX365151 AX20106 653 100.0 915 6 AX267860 AX365151 AX20106 653 100.0 1012 6 AX369151 AX20689 AX36515 6 AX369165	æ		ė.	83		5148	∞ י	-,
653 100.0 6 AX355960 AX355960 653 200.0 6 AX355960 653 100.0 915 6 AR400544 AR405811 653 100.0 915 6 AR400544 AR405811 AX201061 653 100.0 915 6 AR201061 AX201061 AX201061 653 100.0 915 6 AX201061 AX201061 AX201061 653 100.0 915 6 AX201061 AX201061 AX201061 653 100.0 915 6 AX305958 AX305948 AX305948 AX305948 AX305948 AX305948 AX305948 AX305948 AX305941 AX305948	σ		ö.	о О		5069	on 1	٠.,
653 100.0 915 6 AR261281 AR261281 AR261281 AR40542 653 100.0 915 6 AR405811 AX261286 AX201061 AX369151 AX369151 AX369151 AX369151 AX369151 AX369165	10		ė.	0		5596	9	•,
653 100.0 915 6 AR400544 AR40054 653 100.0 915 6 AR201061 653 100.0 915 6 AR201061 653 100.0 915 6 AR201061 653 100.0 1012 6 AR2020689 653 100.0 1012 6 AR369165 653 100.0 1155 6 AR369165 653 100.0 1203 6 AR400556 653 100.0 1203 6 AR400556 653 100.0 1203 6 AR400556 653 100.0 1203 6 AR203038 653 100.0 1464 6 AR322018 653 100.0 1557 6 AR323018 653 100.0 1557 6 AR323018 653 100.0 1557 6 AR323018 653 100.0 1578 6 AR321946 653 100.0 1578 6 AR321946 653 100.0 1578 6 AR321946 653 100.0 1578 6 AR321946 653 100.0 1578 6 AR312091 653 100.0 1752 6 AR316059	11		ö	91		28	oo ·	•2
653 100.0 915 6 AR405811 AR405811 ARX201061 653 100.0 915 6 AR201061 ARX201061 653 100.0 915 6 AR201061 AR207064 AR227764 653 100.0 915 6 AR307151 AR207068 653 100.0 1012 6 AR305958 AR400852 653 100.0 1203 6 AR405823 AR40085 AR40085 653 100.0 1203 6 AR405823 AR40085 AR40085 653 100.0 1203 6 AR204010 AR229410 AR229410 AR322941 AR30695 AR30695 AR30695 AR30695 AR30695 AR30695 AR30695 AR30696 AR	12		ė.	91		54	ማ ፣	٠, ,
653 100.0 915 6 AX201061 AX20106 653 100.0 945 6 AX201061 AX267046 653 100.0 1012 6 AX369151 AX36915 653 100.0 1012 6 AX36999 AX36595 653 100.0 1012 6 AX369165 AX36916 653 100.0 1203 6 AX369165 AX36916 653 100.0 1203 6 AX405823 653 100.0 1203 6 AX201078 AX36916 653 100.0 1203 6 AX201078 AX36204 653 100.0 1464 6 AX220410 AX22041 653 100.0 1464 6 AX322028 AX405829 653 100.0 1464 6 AX322028 AX36294 653 100.0 1464 6 AX322028 AX36195 653 100.0 1464 6 AX361955 AX35204 653 100.0 1557 6 AX322028 AX35204 653 100.0 1557 6 AX322016 AX35203 653 100.0 1578 6 AX361939 AX315608 653 100.0 1578 6 AX31696 AX15618 653 100.0 1578 6 AX31698 AX31698 653 100.0 1578 6 AX31698 AX31698 AX31698 653 100.0 1752 6 AX31698 AX31698 AX31698 653 100.0 1752 6 AX31698 AX31698 AX31698 653 100.0 1752 6 AX316989 AX316304 653 100.0 1752 6 AX316989 AX316984 AX316804 653 100.0 1752 6 AX316989 AX316984 AX316984 AX316984 AX316808 AX316984 AX316988 AX316984 AX316884 AX316884 AX316884 AX316884 AX316	13		ė.	91		8		,,
653 100.0 915 6 AX267860 AX26786 653 100.0 945 6 AX369151 AX36786 653 100.0 1012 6 AX26689 AX365915 653 100.0 1012 6 AX365958 AX365915 653 100.0 1012 6 AX365958 AX365916 653 100.0 1203 6 AX405823 AX405823 653 100.0 1203 6 AX405823 AX26107 653 100.0 1203 6 AX267877 AX26107 653 100.0 1203 6 AX267877 AX220107 653 100.0 1464 6 AX322028 AX22687 653 100.0 1464 6 AX156105 AX22201 653 100.0 1557 6 AX361955 AX36195 653 100.0 1557 6 AX322016 AX36193 653 100.0 1578 6 AX322016 AX36193 653 100.0 1578 6 AX316986 AX316986 AX316986 653 100.0 1752 6 AX322011 AX322011 AX321941 AX321941 AX322014 AX321941 AX3	14		90	6		9	o١	٠, ،
653 100.0 945 6 AX2369151 AX369153 653 100.0 945 6 AX369155 653 100.0 1012 6 AX220689 AX36595 653 100.0 1012 6 AX365958 AX36595 653 100.0 1155 6 AX3659165 AX40655 653 100.0 1203 6 AX406556 AX40655 AX40655 653 100.0 1203 6 AX207078 AX226787 AX267877 653 100.0 1203 6 AX207078 AX267877 AX267878 653 100.0 1464 6 AX156105 AX156105 AX156105 AX156105 AX156105 653 100.0 1557 6 AX156109 AX26797 AX36195 AX26797 AX36195 AX156109 AX15	15		9	91		982	o,	,, .
653 100.0 945 6 AR359151 AA359151 653 100.0 1012 6 AR365968 AX365958 653 100.0 1012 6 AX365968 AX365958 653 100.0 1105 6 AR405823 653 100.0 1203 6 AR405823 653 100.0 1203 6 AR2020178 AR405823 653 100.0 1203 6 AR202018 AR202010 653 100.0 1464 6 AR229410 AR229410 653 100.0 1464 6 AR322018 AR20203 653 100.0 1464 6 AR322018 AR32203 653 100.0 1464 6 AR322016 AR32203 653 100.0 1557 6 AR322016 AR32203 653 100.0 1557 6 AR322016 AR32203 653 100.0 1578 6 AR322038 AX36193 653 100.0 1578 6 AX36199 AX36195 653 100.0 1752 6 AX36199 AX36196 653 100.0 1752 6 AX361999 AX36196	16		2.5	40.		9 5	4 F	
653 100.0 1012 6 AX365958 6 533 100.0 1155 6 AX365958 6 533 100.0 1155 6 AX365958 6 533 100.0 1203 6 AR400556 653 100.0 1203 6 AR400556 653 100.0 1203 6 AX26787	17		9 6	2, 4		1 2	n a	
653 100.0 1012 6 AX369368 AX369398 AX369398 653 100.0 1155 6 AX400565 653 100.0 1203 6 AX400565 653 100.0 1203 6 AX267978 AX267877 653 100.0 1203 6 AX267978 AX267877 AX267877 653 100.0 1203 6 AX26797 AX267877 AX36195 AX26787 AX36195 AX36199 AX	80 1			107		9 5	DΙ	•
653 100.0 1203 6 AR405826 663 100.0 1203 6 AR405826 653 100.0 1203 6 AR405826 653 100.0 1203 6 AR405826 653 100.0 1203 6 AR267877 AR267877 653 100.0 1203 6 AR267910 AR229410 AR229410 AR3229410 AR3294110 AR3	9 0			101		υ . υ .	nν	
653 100.0 1203 6 AR205026 653 100.0 1203 6 AR201078 AR201078 AR201078 653 100.0 1203 6 AR201078 AR201078 AR20208 653 100.0 1464 6 AR229410 AR229410 653 100.0 1464 6 AR322028 AR322028 AR322028 653 100.0 1464 6 AR329398 AR32203 AR32203 653 100.0 1557 6 AR322016 AR322938 AR32293 653 100.0 1557 6 AR322016 AR32293 AR32293 653 100.0 1578 6 AR322938 AR32293 AR32293 653 100.0 1578 6 AR322946 AR32293 AR32293 AR32293 653 100.0 1578 6 AR329946 AR32293 AR3229413 AR32203 AR3229413 AR32203 AR3229413 AR32203 AR3229413 AR32203 AR3229413 AR322944 653 100.0 1752 6 AR322940 AR3229413	2 6			120		7 4	v	• •
653 100.0 1203 6 AX201078 AX201078 AX201078 653 100.0 1203 6 AX201078 653 100.0 1203 6 AX201078 AX201078 AX201078 653 100.0 1464 6 AX32028 AX30105 653 100.0 1464 6 AX30105 AX30105 AX30105 653 100.0 1557 6 AX30105 AX30105 AX30105 653 100.0 1557 6 AX30105 AX30105 AX30105 653 100.0 1557 6 AX30103 AX30105 AX30105 653 100.0 1578 6 AX30103 AX30105 AX30105 653 100.0 1578 6 AX30105 AX30105 AX30105 653 100.0 1752 6 AX30105 AX30105 AX30105 AX30105 653 100.0 1752 6 AX30105	1 0			7.0		9 6	S	
653 100.0 1203 6 AX267877 AX267877 AX267877 CAX267877 CAX26787 CAX26797	23		000	120		0	~	٠,
653 100.0 1464 6 AR229410 AR229410 653 100.0 1464 6 AR322028 AR322028 653 100.0 1464 6 AR322028 AR322028 653 100.0 1464 6 AR322038 AR325020 653 100.0 1557 6 AR322016 AR32201 653 100.0 1557 6 AR322016 AR32201 653 100.0 1578 6 BD264515 AR32201 653 100.0 1578 6 AR322038 AR32203 653 100.0 1578 6 AR322038 AR32203 653 100.0 1578 6 AR322038 AR32203 653 100.0 1578 6 AR32941 AR32203 653 100.0 1752 6 AR32031 AR32203 653 100.0 1758 6 AR32030 AR36195 653 100.0 1758 6 AR32030 AR36195 653 100.0 1758 6 AR32030 AR36195	24		00	120		787	~	•
653 100.0 1464 6 AR322028 AR322028 AX352028 653 100.0 1464 6 AX361955 AX352028 AX352028 653 100.0 1464 6 AX361955 AX352028 AX355105 653 100.0 1557 6 AR322016 AX32203 AX35203 653 100.0 1557 6 AX32016 AX35203 AX35193 AX35193 AX35193 AX35193 AX35193 AX35194 6 653 100.0 1578 6 AX351946 AX35294 AX35194 6 653 100.0 1578 6 AX351946 AX35194 6 653 100.0 1578 6 AX316986 AX316989 AX316986 AX316986 AX316986 AX316986 AX316986 AX316986 AX316959 AX316986 AX316986 AX316986 AX316986 AX316986 AX316986 AX316988 AX316986 AX316988 AX316988 AX316988 AX316988 AX316988 AX316989 AX316988 AX316888	25		00	146		341	~	٠,
7 653 100.0 1464 6 AX156105 AX156105 8 653 100.0 1557 6 AR22939 AR22939 0 653 100.0 1557 6 AR322016 AR32201 1 653 100.0 1557 6 AX156089 AX15608 2 653 100.0 1578 6 AX261939 AX36193 3 100.0 1578 6 AX361946 AX36193 4 653 100.0 1578 6 AX35193 5 653 100.0 1578 6 AX35193 6 653 100.0 1578 6 AX35193 6 653 100.0 1578 6 AX35193 6 653 100.0 1590 6 AX316199 6 653 100.0 1752 6 AX322941 6 653 100.0 1752 6 AX3619	26		00	146		202	O I	••
653 100.0 1464 6 AR361955 AX361959 653 100.0 1557 6 AR322016 AR322016 AR322016 653 100.0 1557 6 AR322016 AR322016 AR322016 653 100.0 1557 6 AR322016 AR322016 AR322016 653 100.0 1578 6 AR32938 AX361939 AX361939 AX361930	27		00	146		덙	0 1	
653 100.0 1557 6 AR229398 ARX29398 ARX29398 ARX29399 653 100.0 1557 6 AR322016 AR325039 AX36193 653 100.0 1557 6 AX361939 AX36193 AX156093 AX156093 AX156093 AX156093 AX156093 AX156093	28		80	146		6	ഗ	J) (
653 100.0 1557 6 AX322016 AX322016 653 100.0 1557 6 AX322016 AX322016 653 100.0 1557 6 AX361939 AX361939 AX361939 AX361939 AX361939 AX361939 AX361939 AX361930 AX361930 AX361930 AX361930 AX361930 AX361930 AX361930 AX36193 AX36193 AX36193 AX36193 AX31696 653 100.0 1578 6 AX316986 AX316986 AX316986 AX316980 AX316998 AX36193 AX316998 AX36193 AX316998 AX36193 AX316998 AX36193 AX316998 AX36193 AX316998 AX36193 AX156093 AX156093 AX156093 AX156093 AX156093 AX156093 AX156093	50		9	155		m :	л,	,, ,
1 653 100.0 1557 6 AX156089 AX361990 BX361990 BX361939 BX361930 BX	30		00	122			- 9	Sednenc
2 653 100.0 1557 6 AA351939 AA351293 AA351293 653 100.0 1578 6 AR229328 AR229328 AR229328 653 100.0 1578 6 AR229328 AR229328 AR22932 653 100.0 1578 6 AR321946 AR321946 AR321946 AR321946 AR321946 AR321949 AX315599 653 100.0 1578 6 AR3219413 AR229413 AR322941 653 100.0 1752 6 AR32031 AR322941	31		0	155		90	מ כ	ט נו
3 653 100.0 1578 6 BD264515 BD264515 4 653 100.0 1578 6 AR229328 AR321946 6 653 100.0 1578 6 AX351946 AR32194 7 653 100.0 1578 6 AX36195 AX36195 8 653 100.0 1590 6 AX316986 AX31696 9 653 100.0 1752 6 AR329413 AR321694 1 653 100.0 1752 6 AX31699 2 653 100.0 1752 6 AX316195 3 100.0 1752 6 AX316195 AX31519 4 653 100.0 1758 6 AX316195 4 653 100.0 1758 6 AX156019 5 100.0 1758 6 AX156093 AX15605	32		00	155		,	"	מ כ
4 653 100.0 1578 6 AR329328 ARX29328 653 100.0 1578 6 AR32946 AR32945 AX351946 AX351946 AX351946 AX35195946 AX35195946 AX35195946 AX35195946 AX35195946 AX35195946 AX35195949 AX35195949 AX351969 AX316996 AX316996 AX316996 AX316996 AX316996 AX316996 AX31699 AX329413 AX32941 AX32941 AX32941 AX32941 AX32941 AX32941 AX32944 AX3100.0 1758 6 AX35099 AX35195 AX35196 AX35196 AX35196 AX35199 AX352949 AX352940 AX352949 AX352940 AX352940 AX352940 AX352940 AX352940 AX352940 AX352940 AX352940 AX352940 AX352	93		00	157		5	ન (י כ
5 653 100.0 1578 6 AR321946 AR321946 6 653 100.0 1578 6 AX361945 AX361594 8 653 100.0 1578 6 AX316986 AX316194 9 653 100.0 152 6 AX316986 AX316196 9 653 100.0 1752 6 AX329413 AX322941 1 653 100.0 1752 6 AX32031 AX32294 2 653 100.0 1752 6 AX16109 AX36199 3 653 100.0 1758 6 AX329401 AX32940 4 653 100.0 1758 6 AX152019 AX32204 5 653 100.0 1758 6 AX152019 AX15609	34		00	157		32	ν.	ω (
6 653 100.0 1578 6 AX355945 AX355945 AX355949 AX355949 AX36795 AX36795 AX36795 AX36795 AX36795 AX36796 653 100.0 1590 6 AX316986 AX316986 AX316996 653 100.0 1752 6 AX352941 AX22941 AX52941 AX52941 AX36709 AX36195 AX361959 AX36195 AX361959 AX36195	32		00	157		6	<u> </u>	י מני
7 653 100.0 1578 6 AX361795 AX36179 8 653 100.0 1590 6 AX316986 AX31698 0 653 100.0 1752 6 AX3229413 AX22941 1 653 100.0 1752 6 AX322031 AX252041 2 653 100.0 1752 6 AX36109 AX36195 3 653 100.0 1758 6 AX329401 AX36195 4 653 100.0 1758 6 AX322049 AX36294 6 653 100.0 1758 6 AX322019 AX32294 6 653 100.0 1758 6 AX322019 AX32294	36		00	157		5594	4.	သိပ
8 653 100.0 1590 6 AX316986 AX31698 9 653 100.0 1752 6 AX329413 AX32941 1 653 100.0 1752 6 AX32931 AX32941 2 653 100.0 1752 6 AX156109 AX36105 3 653 100.0 1758 6 AX229401 AX32940 4 653 100.0 1758 6 AX320109 AX322940 5 653 100.0 1758 6 AX156093 AX15609	37		00	157		175	ייט	CO (
9 653 100.0 1752 6 AR229413 AR22941 0 653 100.0 1752 6 AR322031 AR32294 2 653 100.0 1752 6 AX36109 AX3650 3 653 100.0 1758 6 AX229401 AX36195 3 653 100.0 1758 6 AR322019 AR322940 5 653 100.0 1758 6 AX36093 AX156093	38		90	156		69	<u>.</u>	Ù (
0 653 100.0 1752 6 AX1322031 AK322021 1 653 100.0 1752 6 AX156109 AX156109 3 653 100.0 1758 6 AX229401 AX36195 4 653 100.0 1758 6 AX229401 AX32294 5 653 100.0 1758 6 AX322019 AX32204 6 653 100.0 1758 6 AX156093	39		00	175		941		ומט
1 653 100.0 1752 6 AXL56109 AXL56109 AX36199 AX36199 AX36199 AX36199 AX26199 AX26199 AX26199 AX26199 AX26199 AX26199 AX26199 AX26099 AX156093 AX156093	4.		. 60	175		200	"	0
653 100.0 1752 6 AX361959 AX36195 653 100.0 1758 6 AX229401 AX22240 653 100.0 1758 6 AX322019 AX322019 653 100.0 1758 6 AX156093 AX15609	41		9	17.		201	٠,	O (
653 100.0 1758 6 AR229401 AR22940 653 100.0 1758 6 AR322019 AR32201 653 100.0 1758 6 AX156093 AX15609	42		00	17		36195	711	מ מ
653 100.0 1758 6 AR322019 AR322019 653 100.0 1758 6 AX156093 AX15609	43		00	175		22940	؛ ب	Ų (
653 100.0 1758 6 AX156093 AX15605	44		Ō			2207	Ξ:	S C
	45		0	7		2609	٠,	

ALIGNMENTS

RESULT 1

AR261272 LOCUS DEFINITION	AR261272 675 bp DNA linear PAT Sequence 822 from patent US 6321716.	29-JAN-2003	
ACCESSION VERSION KEYWORDS	1 GI:280		
E	Unknown. Unknown. Unklassified. 1 (bases 1 to 675) 1 (bases 1 to 675) Mashiki,Z. and Harada,J. Negative pressure control apparatus for engine mounted patent: U6321716-A 822 27-NOV-2001; Location/Qualifiers /organism="unknown"	in vehicle	
ORIGIN	/mol_type="genomic DNA"		
Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	ment Scores: 2.4e-44 Length: 675 No.: 653.00 Matches: 128 int Similarity: 100.00\$ Conservative: 0 Local Similarity: 100.00\$ Mismatches: 0 Match: 6 Gaps: 0		
US-09-684-2	684-215B-18 (1-128) x AR261272 (1-675)	-	
ζζ. Db	1 ThralaalaseraspasnPheGlnLeuserGlnGlyGlyGlyGlnGlyPheala1leProll	eProile 20 CCGATC 81	
SP GS	21 GlyGlnAlaMetAla11eAlaGlyGlnIleLysLeubroThrValHis1leGlyProThr 	YProThr 40 GCCTACC 141	
ος Βb	41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 	nArgval 60 ACGCGTG 201	
ος 15	61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 102 GrCGGGAGCGCTCCGGCGAGAGTCTCGGCATCTCCACCGGCGACGTCATCACGGCGGCGCGCGC	rAlaval 80 cgcggrc 261	
55 QG	81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 	SHISPro 100	
Oy. 1	101 GlyAspVall1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 	yAsnval 120 GAACGTG 381	
\$ \$4 6	121 ThrLeublaGluglyProProAla 128 		
RESULT 2 AR400535 LOCUS DEFINITION ACCESSION	AR400535 675 bp DNA linear PAT N Sequence 822 from patent US 6620922. AR400535 AR400535.1 GI:40144000	18-DEC-2003	
ALTITE	Unknown. Unknown. Unclassified. Usses 1 to 675) Xu, J., Dasses 1 to 675. Xu, J., Day, C., Mitcham, J.L., Harlocker, S.L., Jiang Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C. Vedvick, T.S., Carter, D. Li, S.X., Wang, A., Skeiky, Y.A., Hepler, M.T. and Henderson, R.A. Compositions and methods for the therapy and diagnosis	,Y., .H., i, of prostate	

|--|

cancer
JOURNAL Patent: US 6620922-A 822 16-SEP-2003;
FEATURES Location/Qualifiers
1. .675
/organism="unknown"
/mol_type="genomic DNA"

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT 29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu.J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stelky,Y.A., Wang,A. and Meagher,M.J. Compositions and methods for the therapy and diagnosis of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                            101 GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                       AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                       322 GGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCACGCGTACAGGGAACGTG 381
                                                                                                                                                                                                                                                                                      GTCGGGAGCGCTCCGGCGGCAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCCGCTC 261
                                                                                                                                                                    GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 141
                                                                                                                                                                                                                            GCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCGCACGAGTCCAACGCGTG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Memo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                         41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
                                                                                                                                                                                                                                                                 80
                                                                                                20
                                                                                                               GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlyGheAlaIleProIle
                                                                                                                                                                                                                                                                 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                ThralaalaaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       675
0
0
0
0
  0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent: WO 0151633-A 679 19-JUL-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .675
/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AX201049 679 from Patent WO0151633.
AX201049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-675)
                                                                    (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-18 (1-128) x AX201049
                                                                    US-09-684-215B-18 (1-128) x AR405802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AX201049.1 GI:15390857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.4e-44
653.00
100.00%
100.00%
 100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                              202
                                                                                                                                                       21
                                                                                                                                                                                   82
                                                                                                                                                                                                                                        142
                                                                                                                                                                                                                                                                                                                          81
                               Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
AX201049
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                8 B 8
                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                      ∂
                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                         g
                                                                                                                                                                                Db
                                                                                                                                                                                                     8 6
                                                                                                ò
                                                                                                                                                       ઠે
```

QY 21 GlyGlnAlaMetAlaTleAlaGlyGlnIleLySele By GGGGAGGGGATGGGGACGCGCCGGGCCCGAGACCAGCCAG	Individual
Db 82 GGGCAGGCGAGGCGAGGCGCCGGGCCCGGGCCCGGGCCCGGGCCCGGGCCCGGGCCCGGCGC	### Second And And And And And And And And And A
Qy 41 AlaPheLeuGlyLeuGlyValValValAspAsnA Db 142 GCCTTCCTCGGCTTGGGTTGTCGGCACACACACACACACA	alvalAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 6
Db 142 GCCTTCCTCGGCTTGGGGTTGTTCGACAACACA Cy (1)	syricicidicalacalcicalcaccaccacicalcaccaccaccaccaccaccaccaccaccaccaccacc
OY 1	AlaSerLeuGlylleSerThrGlyAspVallleThrAlaVal 8
Oy 101 GlyAspValileSerValThrTrpGlnThrI Oy 101 GlyAspValileSerValThrTrpGlnThrI Db 322 GGTGACGTCATCTCGGTGACCTGGCAACCGCAACCGCAACCACGACGAACCACGTACGT	SeralaThralaMetalaAspAlaLeuAsnGlyHisHisPro 1 [
QY 101 GlyAspValleSerValThrTrpGlnThrI Db 322 GGTGACGTCATCTCGGTGACCTGGCAAACCP QY 121 ThrLeuAlaGluGlyProProAla 128 Db 382 ACATTGGCCGAGGACCCCCGGCC 405 RESULT 5 AX267848 LOCUS CCCCCGGCC 405 AX267848 LOCUS ACCESION AX267848.1 Glil6516494 VEEVANDDS SOURCE Homo sapiens ORGANISM WEMMALISM AX267848.1 Glil6516494 VEEVERING NAMMALISM AX267848.1 Glil6516494 VEEVANDDS SOURCE Mammalia; Butheria; Primates; Car Mammalia; Butheria; Primates; Car Mammalia; Butheria; Primates; Car AUTHORS Xu, J, Dillon, D.C., Mitcham, J.L., Vedvick, T.S., Carter, D., Li,S.X. AUTHORS AUGOSTIONS and methods for the Cancer JOURNAL CORIXA CORPORATION (US) FEATURES SOURCE FACTORES FORTING ALIGNMENT SCORES: 1. 675 OCNEG Dest Location/Qualifiers Incomplete "unassigned DI Ab_Xref="taxon:9606" Dest Location/ON9* Mismal Query Match: Best Location Gaps: US-09-684-215B-18 (1-128) x AX267848 (1-675)	ThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 1
Cy 121 ThrLeuhlaGludlyProProAla 128 Cy 121 ThrLeuhlaGludlyProProAla 128 Db 382 ACATTGGCCGAGGGACCCCGGGC 405 RESULT 5 AX267848 LOCUS DEFINITION SEQUENCE 822 from Patent WO017303 ACCESSION AX267848.1 G1:6516494 VERNORDS SOURCE ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) AUTHORS XLU, Dillon, D.C., Mitcham, J.L., Xalos, M.D., Fanger, G.R., Stetter, D., Li, S.X., and Henderson, R.A. TITLE Compositions and methods for the cancer and Henderson, R.A. TITLE Compositions and methods for the cancer woolf of the corganisms—"Homo sapiens (molitiers source cancer woolf of the corganisms—"Homo sapiens (molitiers source cancer similarity: 100.00% Match bercent Similarity: 100.00% Misma Query Match: 653.00 Dest Local Similarity: 100.00% Misma Query Match: 653.00 US-09-684-215B-18 (1-128) x AX267848 (1-675)	ACCTGGCAAACCAAGTCGGCGGCACGCGTACAGGGAACGTG 3 ProAla 128
PESULT 5 RESULT 5 AX267848 LOCUS DEFINITION Sequence 822 from Patent W0017303 ACCESSION AX267848.1 GI:16516494 VERYORDS SOURCE Homo sapiens ORGANISM Mammalia; Eutheria; Primates; Cra AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Vedvick,T.S., Carter,D., Li,S.X., AUTHORS AND SHORD SHORD SHORD SHORD SHORD FEATURES SOURCE JOURNAL Patent: W0 0173032-A 822 04-OCT-: CORIXA CORPORATION (US) FEATURES SOURCE JOURNAL Patent: W0 0173032-A 822 04-OCT-: CORIXA CORPORATION (US) FEATURES SOURCE JOURNAL Patent: W0 0173032-A 822 04-OCT-: CORIXA CORPORATION (US) FEATURES LOCATION (US) LOCATION SAPIENS No: SOURCE ALIGNMENT SCORES: CORGANISM="Homo Sapiens" MIGHAND ALIGNMENT SCORES: CORGANISM="Homo Sapiens" MOI LYPE="Unassigned DI ADS. XICHE="LAXON:9606" DEFINITION: MATCH: GESSION GONES DEFINITION: MATCH: GONES DEFINITION: M	froala 128
RESULT 5 AX267848 LOCUS DEFINITION Sequence 822 from Patent W0017303 ACCESSION AX267848 I GI:16516494 KEWORDS Homo sapiens Eukaryota; Home sapiens CORGANISM Homo sapiens Eukaryota; Home sapiens FU, J., Dillon, D. C., Mitcham, J. L., Vad'ick, T. S., Carter, D., Li, S. X., and Henderson, R.A. TITLE COMPOSITIONS and methods for the cancer JOURNAL CORRIXA CORPORATION (US) FEATURES Incation/Qualifiers CORRIXA CORPORATION (US) FEATURES Incation/Qualifiers Alignment Scores: CORGANISM: Home sapiens Antignment Scores: CORGANISM: Length Score: CORGANISM: Match Score: CORGANISM: Home sapiens Antignment Scores: CORGANISM: Home sapiens Antig	675 bp DNA linear PAT 26-OCT-2 494 Chordata; Craniata; Vertebrata; Buteleostomi Primates; Catarrhini; Hominidae; Homo. Mitcham,J.L., Harlocker,S.L., Jiang,Y., R., Retter,M.W., Stolk,J.A., Day,C.H., D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,P.
ORGANISM Home sapiens (name) ORGANISM Home sapiens Bukaryota; Metazoa; Chordata; Cra Mammalia; Eutheria; Primates; Cat Mammalia; Eutheria; Primates; Cat Matthors, M.J., Dillon,D.C., Mitcham,J.L., Vedvick,T.S., Carter,D., Lis.x., Vedvick,T.S., Carter,D., Lis.x., and Henderson,R.A. TITLE Compositions and methods for the cancer DOURNAL Patent: Detert: WO 0173032-A 822 04-OCT-: CORIXA CORDEATION (US) FEATURES 1. 675 Source ORIGIN Alignment Scores: Pred. No.: Pred. No.: Pred. No.: Percent Similarity: DO.:004 Misma Query Match: 653.00 Conse Best Local Similarity: DB:: 663.00 Conse Best Local Similarity: DB:: 670.004 Conse Best Local Similarity: DB:: 740.005	Chordata; Craniata; Vertebrata; Buteleostomi; Primates; Catarrhini; Hominidae; Homo. Mitcham,J.L., Harlocker,S.L., Jiang,Y., .R., Retter,M.W., Stolk,J.A., Day,C.H., .D., Li,S.X., Wang,A., Skelky,Y.A., Hepler,W.
REFERENCE 1 AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Kalos, M.D., Fanger, G.R., Retter, P. Vedvick, T.S., Carter, D., Li,S.X., and Henderson, R.A. TITLE compositions and methods for the cancer JOURNAL Patent: WO 0173032-A 822 04-OCT-; CORIXA CORPORATION (US) FEATURES 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1673 1	Mitcham,J.L., Harlocker,S.L., Jiang,Y., .R., Retter,M.W., Stolk,J.A., Day,C.H., ,D., Li,S.X., Wang,A., Skelky,Y.A., Hepler,W.
TITLE Compositions and methods for the cancer JOURNAL Patent: WO 0173032-A 822 04-OCT-: CORIXA CORPORATION (US) FEATURES Location/Qualifiers Location/Qualifiers Location/Qualifiers /Organism="Homo sapiens /mol_type="unassigned Di /db_xref="taxon:9606" Alignment Scores: Pred. No.: Score: Pred. No.: Score: Pred. No.: Score: Percent Similarity: 100.00\$ Petroset Similarity: 100.00\$ Conses Best Location Similarity: 100.00\$ Conses Conses Conses Best Location Similarity: 100.00\$ Conses Conses Conses Conses Best Location Similarity: 100.00\$ Conses	
E: WO 0173032-A 822 0x A CORPORATION (US) Location/Qualifies Location/Qualifies Location/Qualifies Location/Gualifies Amol Lype="unassig/db_xref="taxon:99" Ab_xref="taxon:99" C3.4e-44 C3.4e-44 C3.4e-44 C3.4e-44 C3.4e-44 C3.4e-44 C3.4e-44 C4.4e-44 C5.4e-44 C5.4e-44 C6.00% C1.128) x AX267848 (C1.128)	ons and methods for the therapy and diagnosis of prostate
1675 /organism="Homo sa/mol_trype="umassiz" /db_xref="taxon:99/db_xref="taxon:99/s: 2.46-44 653.00 y: 100.00\$ rity: 100.00\$ f(1-128) x AX267848 ((O 0173032-A 822 04-OCT-2001; RPORATION (US) Location/Qualifiers
2.4e-44 653.00 ricy: 100.00% ricy: 100.00% 6 (1-128) x AX267848 (1675 //organisma="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
2.4e-44 653.00 rity: 100.00% fity: 100.00% 6 (1-128) x AX267848 (•
-09-684-215B-18 (1-128) x AX267848 (1-67	2.4e-4 653.00 100.00 100.00
	848 (1-67
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSer(ThralaalaseraspasnPheGlnLeuserGlnGlyGlyGlnGlyPhealaileProile 20
Oy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle	GlyGlnAlaMetAlaileAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
DD 82 GGGCAGGCGATGGCGATCGCGGGCCCAGATC	-
Oy 41 AlaPheLeuGlyLeuGlyValValAppAsn	AlaPheLeuGlyLeuGlyValValAspAspAspAshGlyAsnGlyAlaArgValGlnArgVal

```
IS 1

IS Mang, T., Watanabe, Y., Henderson, R.A., Johnson, J.C., Retter, M.W., Marnerakis, M., Carter, D., Fanger, G.R., Vedvick, T.S., Bangur, C.S., Manabb, A., Fanger, N., Switzer, A., Mcneill, P.D. and Clapper, J.D. Compositions and methods for the therapy and diagnosis of lung cancer WO 0204514-A 1862 17-JAN-2002;

LORIXA CORPORATION (US)

S. Location/Qualifiers

Lorization/Qualifiers

Jorganism="Homo sapiens"

/mol type="unassigned DNA"

/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-FEB-2002
                                                                                                      16-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAT
                                                                                                       PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
7
0
0
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                    AX369152 822 bp DNA Sequence 1862 from Patent WO0204514. AX369152 GI:18857170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       894 bp
Patent WO0196390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-18 (1-128) x AX369152 (1-822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrieuAlaGluGlyProProAla 128
              2.95e-44
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AX351489
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
AX351489
LOCUS
DEFINITION
                                                                     RESULT 7
AX36152
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 6 8 6 8 6 8 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ♂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                   Unknown.

ISM Unknown.

Volassified.

VCE 1 (bases 1 to 822)

ORS Wang, T. Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,

ORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

Carter, D., Retter, M.W., Mannion, J., Fan, L.

Carter, D., Retter, M.W., Mannion, J., Fan, L.

Carter, D., Retter, M.W., Mannion, J.

Carter, D., Retter, M. A.

Carter, D
                                                                                                                                                                                                                                                                                                     PAT 10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyAspVall1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                82 GGGCAGGCGATGGCGATCGCGGGCCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321
                         ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
                                                                                      AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCGGGAGCGCTCCGGCGGCAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASPGIYAIAProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHioPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                         GACGGCCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAACGGGGCATCATCCC
GCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGAGCGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
0
0
0
0
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                     bp DNA
6509448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-822)
                                                                                                                                                                                                                            ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                            ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                    822 |
Sequence 1862 from patent US -
AR277645
AR277645.1 GI:29711294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-18 (1-128) x AR277645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.95e-44
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
                                                                                    81
142
                         61
                                                        202
                                                                                                                   262
                                                                                                                                                  101
                                                                                                                                                                                322
                                                                                                                                                                                                            121
                                                                                                                                                                                                                                           382
                                                                                                                                                                                                                                                                       RESULT 6
AR277645
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOUNCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ठ व ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Бb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                   음 장
                                                                                                           qq
                                                                                                                                                                          q
                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                         셤
                     ò
                                                                                                                                                  ò
```

40

20

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

FEATURES SOURCE

JOURNAL

REFERENCE AUTHORS TITLE

Patent: WO 0200174-A 353 03-JAN-2002;
CORIXA CORPORATION (US)
Location/Qualifiers
1. :900
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606" DNA AX365960 900 bp D Sequence 353 from Patent W00200174. AX365960.1 GI:18697458 Length: US-09-684-215B-18 (1-128) x AR220690 (1-900) 121 ThrLeuAlaGluGlyProProAla 128 3.24e-44 653.00 100.00% 100.00% 3.24e-44 Score:
Percent Similarity:
Best Local Similarity:
Query Match: Alignment Scores: Pred. No.: Alignment Scores: Pred. No.: AX365960 LOCUS LOCUS DEFINITION ACCESSION VERGION KEYWORDS SOURCE ORGANISM 1 JOURNAL FEATURES SOURCE source REFERENCE AUTHORS JOURNAL FEATURES TITLE ORIGIN 셤 ठ हे ठ 8 8 8 8 6 8 8 & 8 8 Unclassified.

(bases 1 to 900)

Wang,T., Fan,L., Kalos,M.D., Bangur,C.S., Hosken,N.A., Fanger,G.R., Li,S.X., Wang,A., Skeiky,Y.A.W., Henderson,R.A. and McNeill,P.D.
Compositions and methods for the therapy and diagnosis of lung cancer 26-SEP-2002 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80 ASPGIVAIAPTOILEASNSETAIATHTAIAMETAIAASPAIALEUASNGIVHISHISPTO 100 20 81 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Jiang,Y., Hepler,W.T., Clapper,J.D., Wang,A. and Secrist,H. Compositions and methods for the therapy and diagnosis of colon cancer 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle 22 ACGGCCGCGTCCCGATAACTTCCCACTGTCCCAGGGTGGGCAGGATTCGCCATTCCCATC PAT Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 900 bp DNA US 6426072. PACENT: WO 0196390-A 236 20-DEC-2001;
CORIXA CORPORATION (US)
LOCATION/QUALIFIERS
1. .894
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606" US-09-684-215B-18 (1-128) x AX351489 (1-894) 121 ThrLeuAlaGluGlyProProAla 128 AR220690 Sequence 353 from patent ar220690 AR220690.1 GI:23327471 AX351489 AX351489.1 GI:18616835 3.21e-44 653.00 100.00% 100.00% Homo sapiens (human) Homo sapiens Percent Similarity: Best Local Similarity: Query Match: DB: Unknown. Unknown. Alignment Scores: Pred. No.: Score:

61 202 81 262

ò g à 셤 8 셤 ò

g &

ò g à q

Mang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A., Moneill,P.D., Fanger,N., Retter,W.W., Marnerakis,M., Fanger,G.R., Vedvick,T.S., Carter,D., Watanabe,Y. and Peckham,D.W. Compositions and methods for the therapy and diagnosis of lung PAT 15-FEB-2002 Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 82 GGGCAGGCGATGGCGATCGCGGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyABpValIleThrAlaVal linear 900 128 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: Patent: US 6426072-A 353 30-JUL-2002; Location/Qualifiers 1. 900 /organism="unknown" /mol_type="genomic DNA"

100

321

261

80

201

9

141

40

20

120 381

RESULT 9
AR226690
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE AUTHORS

TITLE

Oy 41 AlaPheLeuGlyLeuGlyValValAsp&	Db 262 GACGGCGCTCCGATCAACTCGGCCACCC Oy 101 GlyAspVallleSerValThrTrpGln' Db 322 GGTGACGTCATCTCGGTGACTGGCAA OY 121 ThrieualaGluGlyProproAla 12	38 12 44 TION IION N DS	SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 915) AUTHORS Xu, J. Dillon,D.C., Mitcham,J Kalos,M.D., Fanger,G.R., Rett Vedvick,T.S., Carter,D., Li,S Vedvick,T.S., Carter,D., Li,S Hepler,W.T. and Henderson,R.A.	TITLE Compositions and methods for cancer JOURNAL Patent: US 6620922-A 834 16-S FEATURES 1. 915 Source / organism="unknown" /mol_type="genomic D	ignment Scor ed. No.: ore: rcent Simila st Local Sim ery Match: :	Oy 1 ThralaalserAmpAsnPheGlnLeu	Oy 61 ValGlySerAlaProAlaAlaSerLeu
rcent Similarity: 653.00 Matches: 128 rcent Similarity: 100.00% Conservative: 0 st Local Similarity: 100.00% Mismatches: 0 ery Match: 100.00% Indels: 0 cery Match: 6 Gaps: 0 -09-684-215B-18 (1-128) x AX365960 (1-900) 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProlle	TAACTTCCAGCTGTCCCAGGGCAGGGATTCGCCATTCCGATC AllealaclyCln1leLySLeuProThrValHis1leGlyProThr	dddigrifiaedd oalaalaserleudly 	Oy 101 GlyaspVallleSerValThrTrpGlnThrLyaSerGlyGlyThrArgThrGlyAsnVal 120		ORGANISM Unknown. Unclassified. Unclassified. REFERENCE 1 (bases 1 to 915) AUTHORS Mashiki, Z. and Harada, J. TITLE Negative pressure control apparatus for engine mounted in vehicle JOURNAL Patent: US 6321716-A 834 27-NOV-2001; FEATURES 1.0915 Source 1.0915 /mol_type="genomic DNA"	<pre>nut Scores: 3.29e-44</pre>	Oy Intralabsensepanthesinesconsistiviting the control of the contr

linear PAT 18-DEC-2003 100 120 ,J.L., Harlocker,S.L., Jiang,Y., tter,M.W., Stolk,J.A., Day,C.H., ,S.X., Wang,A., Skeiky,Y.A.W., r the therapy and diagnosis of prostate 141 201 261 rAlaMetalaAspAlaLeuAsnGlyHisHisBro 100 40 09 80 261 80 paenasnglyasnglyaladrgvalglnargval 60 81 20 euserGlnglyGlyGlnGlyPheAlatlePro1le nralametalaaspalaLeuasnGlyHisHisPro nThriysSerglyGlyThrArgThrGlyAsnVal uGlylleSerThrGlyAspVallleThrAlaVal 915 0 0 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: 5 bp DNA 6620922. 6-SEP-2003; -915) DNA"

```
PAT 26-OCT-2001
                                                                                                                          Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retrer, M.W., Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J. Compositions and methods for the therapy and diagnosis of prostate cancer.

Patent: WO (151633-A 691 19-JUL-2001;
CORIXA CORPORATION (US)

1. 915

/ corganism="Homo sapiens"
// mol type="unassigned DNA"
// db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
           PAT 29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                               21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLySLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 AlaPheieuGlyJeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
           linear
                                                                                                                                                                                                                                                                                                                      915
1128
0
0
0
                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AX267860 915 bp
Sequence 834 from Patent WO0173032.
AX267860
AX267860.1 GI:16516503
             915 bp I
WO0151633.
                                                                                                                                                                                                                                                                                                                                                                                                           (1-915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-18 (1-128) x AX201061
                       691 from Patent
                                               AX201061.1 GI:15390868
                                                                                                                                                                                                                                                                                                                      3.29e-44
653.00
100.00%
100.00%
                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                         Sequence t
                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
AX267860
LOCUS
DBFINITION
ACCESSION
VERGION
KEYWORDS
SOURCE
ORGANISM
AX201061
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
VERYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                      source
                                                                                                                       REFERENCE
AUTHORS
```

us-09-684-215b-18.rge

/organism="unknown" /mol_type="genomic DNA"	Alignment Scores: 3.41e-44 Length: 945 Pred. No.: 653.00 Matches: 128 Score: 563.00 Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 100.00\$ Mismatches: 0 DB: 6	-09-684-2	и—U н—b	Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValileThrAlaVal 80			Qy 121 ThrLeuAlaGluGlyProProAla 128 Db 382 ACATTGGCCGAGGGACCCCCGGCC 405	RESULT 17 AX369151 AX369151 945 bp DNA linear PAT 16-FEB-2002 DEFINITION Sequence 1861 from Patent WO0204514.	ACCESSION AX369151 VERSION AX369151.1 GI:18857169 KEYWORDS . SOUNCE Home appiens (human)		AUTHORS Wang,T., Watanabe,Y., Henderson,R.A., Johnson,J.C., Retter,M.W., Marnerakis,M., Carter,D., Fanger,G.S., Bangur,C.S., Monabb,A., Fanger,N., Switzer,A., Monelll,P.D. and Clapper,J.D. TITLE Compositions and methods for the therapy and diagnosis of lung		<pre>source 1945 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</pre> ORIGIN	Alignment Scores: 3.41e-44 Length: 945 Pred. No.: 653.00 Matches: 128 Score: 653.00 Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0
REFERENCE 1 AUTHORS XL, J. Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,		<pre>source 1915 // Organism="Homo sapiens" // mol_type="unassigned DNA" // db_xref="taxon:9606"</pre>	nment Scores: No.: 65.00 ent Similarity: Local Similarity: 100.00\$ y Match: 60.00\$	US-09-684-215B-18 (1-128) x AX267860 (1-915) QY	21 GlyglnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisTleGlyProThr 	41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 	61 ValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspValIleThrAlaVal 	81 AspGlyalaProlleAsnSeralaThrAlaWetAlaAspAlaLeuAsnGlyHisHisPro	Qy 101 GlyAspValI1eSerValThrTxpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120 	Qy 121 ThrLeuAlaGluGlyProProAla 128 Db 382 ACATTGGCCGAGGACCCCGGCC 405	AR277644 945 bp	N Sequence 1851 from parent US 650949 AR277644 AR277644.1 GI:29711293	SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE I (bases 1 to 945) AUTHORS Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S.,	Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A. TITLE Compositions and methods for the therapy and diagnosis of lung cancer JOURNAL Patent: US 6509448-A 1861 21-JAN-2003; FEATURES Location/Qualifiers source 1. 945

us-09-684-215b-18.rge

Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAslaArgValGlnArgVal 60 Db 187 GCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCGACGAGGCACGAGTCCAACGGGGG 246 Qy 61 ValGlySerAlaProAlaAlaSerLeuGly11eSerThrGlyAspValI1eThrAlaVal 80 80 247 GTCGGGAGCGCTCCGGCGCAAGTCTCCACCGCGACGTGATCACCGCGGTC 306 30 Qy 81 AspGlyAlaPro11eAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100 Db 307 GACGGCGCTCCGATCACGCCACCGCGATGACGCGTTAACGGCATCATCCC 366 Qy 101 GlyAspValI1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120 Db 367 GGTGACGTCTCGGTAACCTGGCAAACCAAGTCGGGCACGCGTACAGGGAACTGTG 426 Qy 121 ThrLeuAlaGluGlyPrOPFOAla 128 Qy 121 ThrLeuAlaGluGlyPrOPFOAla 128 Db 427 ACATGGCCCCGGGGCCCCGGGCCCCGGGCGCCCGTAACGGGAACCTCGGGAACGTAAGGCGAACGTAACAGGCGCACGAGGAACCCCCGGCCCCCGGGCCCCCGTAACAGGCGCCCCCGGCAAGGAACCCCCGGCCCCCCGGCCAAGGAACCCCCGGCCCCCC	RESULT 19 AX365958 LOCUS AX365958 LOCUS DETINITION Sequence 351 from Patent W00200174. ACCESSION AX365958. VERSION KEYWORDS SOURCE HOMO sapiens (human) ORGANISM Homo sapiens DRGANISM Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homo.	Li,S.X., Kalos,M.D., J. r,M.W., Marnerakis,M., abe,Y. and Peckham,D.W the therapy and diagnos and Lagnos	Alignment Scores: 3.66e-44 Length: 1012 Pred. No.: 653.00 Matches: 128 Score: 653.00 Matches: 128 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Mismatches: 0 DB: 6 Gaps: 0	ThralaalaSerAspAsnPhed
Query Match: 100.00% Indels: 0 DB: 6 Gaps: 0 US-09-684-215B-18 (1-128) x AX369151 (1-945) 0 QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyGlnGlyPheAlaIleProIle 20 Db 2 ACGGCCGCTCCGATAACTTCCAGCTGTCCCAGGGGATTCGCCATTCCGATC 81 QY 2 GlyGlnAlaAmetAlaIleAlaGlyGlnIleLySLeuProThrValHisIleGlyProThr 40 Db 82 GGGCAGGCGATCGCGGGCCCAGATCAAGCTTCCCACCGTTCATATCGGGCTACC 141 QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAlaArgValGGCTACCACGGCTACC 141 QY 41 AlaPheLeuGlyLeuGlyLeuGlyAlaAspAsnAsGGCGACGACGACGACGACGACGCGTG 201 Db 142 GCCTTCCTCGGCTTGGGTTTGTCGACAAACGGCGACGACGACGACGACGACGACGACGACGA	Db 202 GTGGGAGGCGTCCGGCGAAGTCTCGGCATCTCCACGGCGACGTGATCACGGCGGTC 261	Db 382 ACATTGGCCGAGGCC 405 RESULT 18 AR220689 LOCUS DEFINITION Sequence 351 from patent US 6426072. ACCESSION AR220689 1 GI:23327470 KEYWORDS SOURCE ORGANISM Unknown: ORGANISM Unknown: Unclassified. REFERENCE 1 (bases 1 to 1012) AUTHORS Wang, T., Fan, L., Kalos, M.D., Bangur, C.S., Hosken, N.A., Fanger, G.R.,	Li,S.X., Wang,A., Skeiky,Y.A.W., Henderson,R.A. and McNeill,P.D. Compositions and methods for the therapy and diagnosis of lung cancer. Patent: US 6426072-A 351 30-JUL-2002; Location/Qualifiers	Alignment Scores: Matches: Conservative: Conservative: Mismatches: Mismatches: Scores: Mismatches: Inc.00* Indels: Gaps: US-09-684-215B-18 (1-128) x AR220689 (1-1012) Oy I ThrAlaAlaSerAspAsnPhedInLeuSerGindlyGlyGlnGlyPheAlaIleProIle 20 I ThrAlaAlaSerAspAsnPhedInLeuSerGindlyGlyGlnGlyPheAlaIleProIle 20 Oy I ThrAlaAlaSerAspAsnPhedInLeuSerGindlyGlyGlnGlyPheAlaIleProIle 20 I

```
Juknown.

ISM Unknown.

ISM Unclassified.

NCE 1 (bases 1 to 1203)

NCE 1 (bases 1 to 1203)

NCE 1 (bases 1 to 1203)

NCE Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.M.

Compositions and methods for the therapy and diagnosis of prostate cancer

Compositions and methods for the therapy and diagnosis of prostate cancer

Location/Qualifiers

1. 1203

Arganism="unknown"

/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAT 18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT 18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AR405823 1 from patent US 6630305.
AR405823 GI:40154660
                                              AR400556 1203 bp DNA Sequence 851 from patent US 6620922. AR400556 AR400556.1 GI:40144037
                                                                                                                                                                                                                                                                                                                                                                                                                        .215B-18 (1-128) x AR400556 (1-1203)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                4.38e-44
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                        Similarity:
al Similarity: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
Unknown.
Unknown.
```

201

9

261

source

ORIGIN

ઠે g ò g

JOURNAL

FEATURES

TITLE

REFERENCE AUTHORS

```
Xu.J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kaloe,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T. and Henderson,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 26-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
Momo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                 ThralaalaseraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1203
                                                                            1203
128
0
0
0
                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parent: WO 0173032-A 851 04-OCT-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .1203
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

    .1203
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AX267877 1203 bp
Sequence 851 from Patent W00173032.
AX267877 AX267877.1 GI:16516515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                              (1-1203)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-684-215B-18 (1-128) x AX201078
                                                                             4.38e-44
653.00
100.00%
100.00%
                                                                                            Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                     202
                                                                                                                                                                                                                                                                                                                                                                                                  262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DECENTION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                    Alignment Sor
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 24
AX267877
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                               DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                       $ 8 $
                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                       원
장
                                                                                                                                                                                                                                                                                 8 8
                                                                                                                                                                                      \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT 29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unclassified.

(bases 1 to 1203)

Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Kalos, M.D., Fanger, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
Hepler, W.T. and Henderson, R.A.

Compositions and methods for the therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                             81
                                                                                                                                                                                                                                                                                                                                                                                       Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                       1203
128
0
0
0
                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: WO 0151633-A 708 19-JUL-2001,
CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                 Cancer
Patent: US 6630305-A 851 07-OCT-2003;
Location/Qualifiers
1. .1203
/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX201078 1203 bp
Sequence 708 from Patent WO0151633.
AX201078 1 GI:15390883
                                                                                                                                                                                                                                                                        (1-1203)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-18 (1-128) x AR405823
                                                                                                                                                                                        4.38e-44
653.00
100.00%
100.00%
                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                            Alignment Scores:
Pred. No.:
Score:
```

101

QQ δ 셤 ઠે

ద ò

95 DP ò 121

RESULT 23
AX201078
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

ORGANISM

REFERENCE AUTHORS

JOURNAL

TITLE

FEATURES

201

80

141 9

40

20 81 261

us-09-684-215b-18.rge

0.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.00	AR322028 TION AR322028 N AR322028 N AR322028 S Unknown. NISM Unknown. NICE 1 (Dass DRS Skeiky, YRY) E Compound Infectio	Source 1.1464 Source 1.1464 Oxganism="unknown" Oxigin	eGinteuSerGinGlyGlyGlnGlyPheAlaileProile 	Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLySLeuProThrValHisIleGlyProThr 40	Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
ore: sr cent Si sr Local ery Matc	81 AspGlyalaProlleAenSerAlaThralaMetalaAspAlaLeuAshGlyHisHisPro 	AR229410 Sequence 3 AR229410 AR229410.1 Unknown. Unknown. Unclassifi I (bases Fling S. F Compounds infection Patent: UC	source 11464 /organism="unknown" /mol_type="genomic DNA"	Alignment Scores: Pred. No.: 5.37e-44 Length: 1464 Score: 653.00 Matches: 128 Secret Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 6 Gaps: 0	US-09-684-215B-18 (1-128) x AR229410 (1-1464) Qy

us-09-684-215b-18.rge

ACCESSION AX361955 VERSION KEYWORDS SOURCE Chlamydia trachomatis SOURCE ORGANISM Chlamydia trachomatis SOURCE ORGANISM Chlamydia trachomatis Bacteria; Chlamydiae; Chlamydiaceae; Chlamydia. REFERENCE 1 AUTHORS Compounds and methods for treatment and diagnosis of chlamydial Infection JOURNAL Patent: WO 0208267-A 348 31-JAN-2002; CORIXA CORPORATION (US) CORIXA CORPORATION (US) FEATURES 1. 1464 / organism="Chlamydia trachomatis" / mol type="unassigned DNA" ORIGIN / db_xref="taxon:813"	Alignment Scores:	4. AlaPheLeudJyLeuGlyValAsphanAshGlyAshGlyAlaArgValGlnArgValGlnArgValGlnArgValGlnArgValGlnArgValGlnArgValGlnArgValGlnArgValGlnArgValGlnArgValGlnArgValGlnArgValGlnArgValGlnArgValGlnArgValGlnArgValGlnArgValGlySerAlaProLaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaValGlyGrGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Qy 101 GlyAspVallleSerValTheThTpGlnThrLysSerClyGlyThrArgThTsTVAJAShTVAL 120 Db 322 GGTGACGTCATCTTGGTTACTTGGTAACCAAGTCGGGCGGCACGCGTACAGGGAACGTG 381 Qy 121 ThrLeuAlaGluGlyProProAla 128 Db 382 ACATTGGCCGAGGGCCCCCGGCC 405	RESULT 29 AR229398 LOCUS DEFINITION Sequence 332 from patent US 6448234. ACCESSION AR229398 VERSION AR229398.1 GI:27268651 KEYWORDS SOURCE UNKNOWN. ONGANISM UNKNOWN. TITLE AUTHORS FINING Sequence 332 from patent US 6448234. REFERENCE I (bases 1 to 1557) AUTHORS FINING Sequence 332 from patent and diagnosis of chlamydial infection JOURNL PERTINGE LOCATION/QUALIFIERS FERTING JOURNL PATURES LOCATION/QUALIFIERS FERTING LOCATION/QUALIFIERS FERTING LOCATION/QUALIFIERS	
Qy 101 GlyAspValIlleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAshVal 120 Db 322 GGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGCGCACGCGTACAGGGAACGTG 381 Qy 121 ThrLeuAlaGluGlyProProAla 128 Db 382 ACATTGGCCGAGGGACCCCCGGCC 405 RESULT 27 AXI56105 1464 bp DNA linear PAT 22-JUN-2001 DEFINITION Sequence 348 from Patent W00140474. ACCESSION AXI56105 1464 bp DNA linear PAT 22-JUN-2001 DEFINITION Sequence 348 from Patent W00140474. AXI56105 ACCESSION AXI56105 AXI56105 SCHENGION AXI56105 AXI56105 Chlamydia trachomatis Chlamydia trachomatis ORGANISM Chlamydiae; Chlamydiae; Chlamydiaceae; Chlamydia.	REFERENCE AUTHORS Probst, P., Bhatia, A., Skeiky, Y.A., Fling, S.P. and Scholler, J. TITLE Compounds and methods for treatment and diagnosis of chlamydial infection JOURNAL Patent: WO 0140474, A98 07-JUN-2001; CORIXA CORPORATION (US) FRATURES Location/Qualifiers 1.1464 NO.1 Lype="unassigned DNA" / db_xref="taxon:813" Alignment Scores: Pred. No.: Score: Score: G53.00 Matches: Percent Similarity: OO.004 CORSENTATION Matches: Descent Similarity: OO.004 CORSENTATION Matches: OO.004 CORSENTATION CORS	7: 100.00\$ Indels: 0 6 Gaps: 0 6 Gaps: 0 7: AXI56105 (1-1464) 1128) x AXI56105 (1-1464) 1138) x AXI56105 (1-1464) 1138-The part of the control of the contro	Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60 Interpretation 142 GCCTTCCTGGTTTGTCGACGGCGACGGCGACGGACGCACGACGGCGACGGCGCACGACG	81 AspGlyA 262 GACGGCG 101 GlyAspV 322 GHINN 121 ThrieuA 382 ACATTGC AX361955	N Sequence 348

source

PAT 17-AUG-2003 ASPGIVALAPTOILGASNSGTALATHTALAMELALAASPALALGUASNGIVHISHISPTO 100 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120 GlyGlnalaMetAlaIleAlaGlyGlnIleLySLeuProThrValHisIleGlyProThr 40 ValGiySerAlaProAlaAlaSerLeuGlyIleSerThrGiyAspValIleThrAlaVal 80 201 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60 22 ACGGCCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC 81 Unknown. Unclassified. 1 (bases) Skeiky,Y.A.W. and Scholler,J. Compounds and methods for treatment and diagnosis of chlamydial GCCTTCCTCGGCTTTGGGGTGTTGTCGACAACAACGGCAACGGCGCACGAACGCGTG ThralaalaserAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAla1leProIle 1557 128 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: AR322016 Sequence 332 from patent US 6565856. AR322016 GI:33707360 June 10 6565856-A 332 20-MAY-2003;
Patent: US 6565856-A 332 20-MAY-2003;
Location/Qualifiers
1. 1557
/organism="unknown"
/mol_type="genomic DNA" US-09-684-215B-18 (1-128) x AR229398 (1-1557) 1. .1557
/organism="unknown"
/mol_type="genomic DNA" ThreuAlaGluGlyProProAla 128 ACATTGGCCGAGGGACCCCCGGCC 405 5.72e-44 653.00 100.00% 100.00% 5.72e-44 653.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: DB: Percent Similarity: Best Local Similarity: Query Match: Unknown. Alignment Scores Pred. No.: Alignment Scores: Pred. No.: 21 82 41 142 19 202 81 262 101 121 RESULT 30
AR322016
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOUNCE
ORGANISM source REFERENCE AUTHORS TITLE JOURNAL FEATURES ORIGIN ð 심 $\stackrel{>}{\circ}$ ď g ò g ò 엄 $\dot{\delta}$ d ઠે ò

US-09-684-215B-18 (1-128) x AR322016 (1-1557)

201 261 100 120 381 141 321 80 9 40 81 142 GCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGAGGTCCAACGCGTG 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 202 GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGGGGTT 81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCGATC 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAanGlyAlaArgValGlnArgVal ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProIle Search completed: April 30, 2004, 02:24:05 Job time : 3674.05 secs ThrieuAlaGluGlyProProAla 128 121 90 A 8 6 6 6 6 8 6 ठ

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

	ņ
OM protein - nucleic search, using frame_plus_pzn model	April 29, 2004, 20:30:12; Search time 364.096 Seconds (without alignments) 1493.479 Million cell updates/sec
M protein	Run on:
Ö	쩦

n on: April 29, 2004, 20:30:12; Seaton Chime 34:090 Seconds (without alignments) 1493.479 Million cell updates/sec		Periect score: b51 Sequence: 1 TAASDNFQLSQGGGFAIPISVTWQTKSGGTRTGNVTLAE 128	Scoring table: BLOSUM62	Xgapop 10.0 , Xgapext 0.5	Ygapop 10.0 , Ygapext 0.5	Fgapop 6.0 , Fgapext 7.0	Delop 6.0 , Delext 7.0
Kull Oll:	Title:	Sequence	Scoring				

3373863 segs, 2124099041 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

N Geneseq 29Jan04:*

1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:* geneseqn2003bs:*geneseqn2003cs:* geneseqn2004s:* geneseqn2002s:* geneseqn2003as:* geneseqn2001bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		tid	tid	cte	tid	cod	cte	cte	cte
	g	Nucleo	Nucleo	Mycoba	Nucleo	DNA en	Mycoba	Mycoba	Mycoba
	Description	Aal40769 Nucleotid	Aa140772	Aaz20206	Aa140770	Abk14140	Aad47078	Aad47077 Mycobacte	Aad28336
	ID	AAL40769	AAL40772	AAZ20206	AAL40770	ABK14140	AAD47078	AAD47077	AAD28336
	DB	. 4	マ	N	4	Q	φ	φ	9
	1	396	672	702	702	702	1002	1002	1002
مد ر	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score		651	651	651	651	651	651	651
	Result No.		7	٣	4	Ŋ	9	7	6 0

8337	ന റ	10771 Nucleoti	40768	26353	47084	28343	0773	1128	0194	7083	8342	5360	29	5358	7110	5357	5355	363	۸,	Ada26361 Mycobacte		nuation (2	403	1466 Myc	4342 Myc	54450 M.	19040 M.	19252 M.	03780	147080 Myc	28339	:91414 Mycobact	91477 Mycobac	
AAD2833 AAX3425	AAX342 AAS037	AAL4077	AAL4076	ADA2635	AAD4708	AAD2834	AAL4077	ABK1412	AAZ2019	AAD4708	AAD2834	ADA2636	ADA2635	ADA2635	AAD4711	ADA2635	ADA2635		ADA2636	ADA2636	AA199682	AAI99683_0	AAT91403	· AAT9146	AAV4434	AAV6445	AAZ1904	AA21925		AAD4708	AAD2833	AAT914	AAT91	AAV443
1002 6 1068 2	~ ~	۵,			_	_			7	_	_	_	_	7	<u>~</u>	m	_	_	₩.	~#	0	0	7	7	7	7	47	47	47	47	47	872	72	872
0.0	0.00	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	9.5	9.5	9.5	9.5	e,	e,	e.	œ.	σ.	9.2	9.2	9.5
ਜਜ	55	17	11 1	11 1	51 1	1 1	1 1	51 1	51 1	51 1	51 1	51 1	51 1	51 1	51 1	51 1	51 1	51 1	51 1	51 1	51 1	51 1	1 6	46	1 6	46	46	46	46	46	94	46	46	94
10	11 12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

ALIGNMENTS

BP. AAL40769 standard; DNA; 396 (first entry) 03-OCT-2002 AAL40769; AAL40769

RESULT 1

Nucleotide sequence encoding Ra12 protein.

Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.

Unidentified.

1.396 /teag= /product= "Ra12 protein" /note= "No start or stop codon" Location/Qualifiers Key

WO200125401-A2

12-APR-2001

06-OCT-2000; 2000WO-US027652.

99US-0158585P 07-OCT-1999;

(CORI-) CORIXA CORP.

```
The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as cources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence
                                                                                                          Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                                                                 Claim 1; Fig 2; 39pp; English
Guderian J;
                                              2001-266299/27.
                                                                   P-PSDB; AAO22138
Skeiky Y,
```

Sequence 396 BP; 68 A; 132 C; 134 G; 62 T; 0 U; 0 Other;

```
396
128
0
0
0
     Length:
Matches:
Conservative:
Mismatches:
Indels:
     9.696-55
651.00
100.00%
100.00%
                               Best Local Similarity:
                      Percent Similarity:
Alignment Scores:
Pred. No.:
                                     Query Match:
DB:
```

```
240
                                                                                                                                                                                                                                                                                                                                                            360
                                                                                                                                                                                                                                                                  IleThralaValaspGlyalaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                             GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                 120
                                                                                                                                                                           180
                         9
                                                                                                                                                                                                        80
                                                                                     21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                               241 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                61 descadescanceceanceceasceanceanceancescaceaccaccaccarcar
                                                                                                                                              41 ileglyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                   121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACAACGGCAACGGCACGA
                                                                                                                                                                                                                                       181 erccaacecereerceeeacecececeeeeacecaceeeaceacececeeeacere
                                                                                                                                                                                                                                                                                                                                                 GGGCATCATCCGGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGGGCACGGT
                                                                                                                                                                                                        ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
US-09-684-215B-23 (1-128) x AAL40769 (1-396)
                                                                                                                                                                                                                                                                                                                                                                                            ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                   a
                                                                                                                                                  ò
                                                                                                                                                                              d
                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                         à
                                                           셤
                                ŏ
```

```
AAL40772 standard; DNA; 672
                             AAL40772
```

(revised)
(first entry) 06-AUG-2003 03-OCT-2002

Nucleotide sequence encoding Ral2-mammaglobin fusion protein.

Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds

Mammalia. Unidentified. Chimeric.

Location/Qualifiers 4. .666 /*tag= a

/*tag= a /product= "Ra12-mammaglobin fusion protein"

WO200125401-A2

06-OCT-2000; 2000WO-US027652.

07-OCT-1999; 99US-0158585P.

(CORI-) CORIXA CORP.

Skeiky Y, Guderian J;

WPI; 2001-266299/27. P-PSDB; AA022141. Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.

Disclosure, Fig 5; 39pp; English

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polymucleotide sequence of Ral2, a 14 Mycobacterium intervalsing a polymucleotide sequence of Ral2, a 14 Mycobacterium tuberculosis, and a heterologous polymucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the fusion polypeptides are useful as cources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polymucleotide sequence represents the DNA encoding the Ral2 on 06-AUG-2003 to correct OS field.)

Sequence 672 BP; 160 A; 185 C; 187 G; 140 T; 0 U; 0 Other;

	672	128	0	0	0	0	
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:	
	1.79e-54	651.00	100.00%	100.00%	100.00%	4	
Allene Scores:	Pred. No.:	Score	Percent Similarity:	Best Local Similarity:	Ouery Match:	DB:	

US-09-684-215B-23 (1-128) x AAL40772 (1-672)

20 84 ThralaalaseraspasnPheGinLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle н 25 ઠે 유

```
ខ្ពង់ខ្ល
                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This DNA sequence includes a coding region for a recombinant Mycobacterium tuberculosis bi-antigen fusion protein (see AAY32071), termed Mb124, composed of the antigens Ra12 and DPDD. The DNA is useful for the recombinant production of the fusion protein. Coding sequences for the antigens were modified by PCR in order to facilitate their fusion and subsequent expression of the fusion protein, and then ligated. The invention provides fusion protein, and then ligated. The invention provides fusion proteins (see ANY32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polymucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective
                                                                                                                                                                                                                                                                                                                                                                                                          100
                                                                                                                                                                204
                                                                                                                                                                                                                                                              264
                                                                                                                                                                                                                                                                                                                                                      ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGGATGGCGGACGCCTTAAC 324
                                                                144
                                                                                                                                                                                                               80
                                                                                                                  9
                       40
                                                         GGGCAAGGCGATGGCGAGACCAGATCCGATCGGGGGGGTCACCCACGTTCAT
                                                                                                                                            ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                              GTCCAACGCGTGGTCGGAAGCGCTCCGGCGGCAAGTCTCGGCGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                               IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis.
                       GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculosis, antigen, fusion protein, Mtb24, Ra12, DPPD, diagnosis, therapy, vaccine, immunogen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis antigen fusion protein Mtb24 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campos-Neto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 ACAGGGAACGTGACATTGGCCGAG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Fig 13A-B; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              品
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US007717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00056556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ20206 standard; DNA; 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skeiky YAW, Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-601610/51.
P-PSDB; AAY32071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09951748-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-APR-1998;
30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ20206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                      85
                                                                                                                       41
                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                205
                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                                                                                                                                                                265
                                                                                                                                                                                                                                                                                                                                                                                                               101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
AAZ20206
AAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                           용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                      g
                                                                                                  8 6 8 6
                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                8
                         ઠે
```

```
85 GGGCAGGCGATGGCGATGGCGGTCGGATCGGTGGGGGGGTCACCCCACCGTTCAT 144
                                                                                                                                                                                                                                                                                                                                                                                                                       265 ATCACCGCGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis;
vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
immunogen; cytokine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                               61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                205 GICCAACGCGIGGTCGGGGGGCGCCGCCGGCAAGICTCGGCAICICCACCGGCGACGGG
                                                                                                                                                                                                   25 ACGGCGCGCTCCGATAACTTCCAGCTGTCCCAGGGTGGCAGGGATTCGCCATTCGATC
                                                                                                                                                                                                                                         21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                      81 IleThralaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
                                                                                                                                                                                     1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaileProIle
immunogens than mixtures of the individual protein components
                        Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence encoding Ral2-DPPD fusion protein.
                                                                707
000
000
000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "Ral2-DPPD fusion protein"
                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                           US-09-684-215B-23 (1-128) x AAZ20206 (1-702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-2000; 2000WO-US027652
                                                            1.88e-54
651.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL40770 standard; DNA; 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORP
                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200125401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
Chimeric.
                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL40770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
```

204

9

20 84 40 264 100

dB;

```
Fusion protein; tuberculosis; Mycobacterium tuberculosis; gene; tuberculostatic; immunogen; vaccine; Ral2-DPPD; Mtb24.
                                                            antigenic fusion protein Ra12-DPPD (Mtb24)
                                                                                                                          Mycobacterium tuberculosis
                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-1997;
01-OCT-1997;
18-FEB-1998;
                                                              DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-DEC-1998;
                        29-AUG-2003
08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SKEI/) S
(DILL/) I
(ALDE/) A
(CAMP/) C
                                                                                                                                       Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REED/)
                                                                                                                                                                                                                                                     S
S
The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 Kbaicon polypeptide, comprising a polynucleotide sequence of Fal2, a 14 Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polymucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCGT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCGACGA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GICCAACGCGIGGICGGGGGCGCICCGGCGAAGICICGGCAICICCACGGGGACGIG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                      Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyBheAlaIleProile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                    Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                          00000
00000
00000
                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-684-215B-23 (1-128) x AAL40770 (1-702)
                                                                                                                          Example 1; Fig 3; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      1.886-54
651.00
100.00%
100.00%
             Guderian J;
                                   WPI; 2001-266299/27.
P-PSDB; AAO22139.
                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
             Skeiky Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
```

```
/partial
/note= "No start for stop codon"
/note= "No start for stop codon"
/transl_except= (pos:1..2, aa:Pro) /transl_except=
(pos:39..41, aa:Xaa) /transl_except= (pos:321..323,
aa:Xaa) /transl_except= (pos:339..341, aa:Xaa)
/transl_except= (pos:450..452, aa:Xaa) /transl_except=
(pos:621..623, aa:Xaa) /note= "No start or stop codon. Xaa= In frame stop codon"
                                                                                                                                                                                                                                                                                                  /partial
/note= "No start or stop codon"
/ransl_accept= (pos:263, c35, aa:Xaa) /transl_except=
(pos:351, c355, aa:Xaa) /transl except= (pos:351, c355, aa:Xaa) /transl_except= (pos:470, c472, aa:Xaa)
/transl_except= (pos:470, c472, aa:Xaa)
/transl_except= (pos:701, 702, aa:Set)
/transl_codon has an apparent 1 nucleotide deletion
which alters the reading frame. Xaa= In frame stop codon"
                                                                                                                                                      transl_except= (pos:694. .696, aa:Xaa)
note= "No start or stop codon. Xaa= In frame stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a purified polypeptide which induces an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New fusion proteins of Mycobacterium tuberculosis antigens, usef diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos-Neto A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky YA, Dillon DC, Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-171134/22.
P-PSDB; AAU74600, AAU76541, AAU76542.
                                                                      *tag= a
product= "Mtb24 #1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= c
/product= "Mtb24 #3"
                                                                                                                                                                                                                                                                               product= "Mtb24 #2"
Location/Qualifiers
1. .702
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example, Fig 13; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-00918112.
97US-00942578.
98US-00025197.
98US-00056556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00287849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REED S G.
SKEIKY Y A.
DILLON D C.
ALDERSON M.
CAMPOS-NETO A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002009459-A1.
```

ThrGlyAsnValThrLeuAlaGlu 128 ACAGGGAACGTGACATTGGCCGAG 408

325 121 385

셤 ò ABK14140 standard; DNA; 702 BP.

WO200272792-A2

```
Mon May
```

```
response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents DNA encoding an M. tuberculosis thusion protein of the invention. This polymucleotide encodes 3 different proteins, each in a different reading frame. (Updated on 29-AUG-2003 to standardise OS field)
```

225 G; 121 T; 0 U; 0 Other; ີ່ວ Sequence 702 BP; 127 A; 229

```
GlyHisHisProGlyAspValIleGerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                264
                                                                                                                                                                                                                                                                                                              324
                                                                                                                                                                                                                      144
                                                                                                                                                                                                                                                   204
                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                        40
                                                                                                                                                                                                                                     9
                                                                                                                                                                            20
                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine, immunity, diagnostic agent; gene therapy, Ra35FLMutSA; mutant; gene; antigen; ds.
                                                                                                                                                                           41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                           IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
                                                                                                                                                                                                                                                    Arcasacctaccacctracacctrassaratracacacaacaacaacaacaacaacaacaa
                                                                                                                                                                                                                                                                  ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis Ra35FLMutSA mutant antigenic protein DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Ra35FLMutSA mutant antigenic protein"
                                                                                                           707
128
0
0
0
                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                              US-09-684-215B-23 (1-128) x ABK14140 (1-702)
                                                                                                                                                                                                                                                                                                                                                          ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                 ACAGGGAACGTGACATTGGCCGAG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
4. .996
/*tag= a
/product= "Ra35FLMuts
                                                                                                                                                                                                                                                                                                                                                                                                      ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                      AAD47078 standard; DNA; 1002
                                                                                                         1.88e-54
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                         385
                                                                                                                                                                                                                                                                                                                                                                                                                    AAD47078;
                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                               265
                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                            325
                                                                                                                                                                                                          27
                                                                                                                                                                                                                        85
                                                                                                                                                                                                                                                     145
                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                  205
                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                           8 8 8
                                                                                                                                                                            8 8
                                                                                                                                                                                                      ठ हे ठ
                                                                                                                                                                                                                                                음 ☆ 음
888666666666888
```

```
The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are microorganisms such as Leishmania and Mycobacterium tuberculosis. Rusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raxising antibodies in a non-human in vivo diagnostic agents and for raxising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis RaisfilmutSA mutant antigenic protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      957
                                                                                                                                                                                              New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 GlyHisHisBroGlyAspVallIeSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1002 BP; 169 A; 331 C; 341 G; 161 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1002
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-23 (1-128) x AAD47078 (1-1002)
                                                                                                                                                                                                                                                                               Disclosure; Page 80-81; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                        <u>ب</u>
                                                                                                                                         Guderian
                                                       13-MAR-2002; 2002WO-US008223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.85e-54
651.00
100.00%
100.00%
                                                                                  13-MAR-2001; 2001US-0275837P
                                                                                                                                        Skeiky Y, Brannon M,
                                                                                                             CORP.
                                                                                                                                                                   WPI; 2002-759844/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                P-PSDB; AAE29703
                                                                                                             (CORI-) CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
DB:
음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 8 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

Mon May

RESULT

717

40

9

657

897

```
GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                            838 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGGCGTTAAC
                                    s98 Aceccececaticalizatiticaecieicaeeaeaeaaeaaaaricecaricear
                                                                        GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                    IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
          ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB32A; Ra32FL; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium sp. MTB32A (Ra35FL) mature protein encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
4. .996
    /*tag= a //trag= a //transl_except= (pos:547. .549, a //transl_except= (pos:550. .552, a
                                                                                                                                                                                                                                                                                                                                                                                                       121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                  958 ACAGGGAACGIGACATIGGCCGAG 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alderson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD28336 standard; cDNA; 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2000; 2000US-00597796.
01-FEB-2001; 2001US-0265737P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2001; 2001WO-US019959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-147798/19.
P-PSDB; AAE17566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky Y, Reed S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200198460-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD28336;
              _
                                                                             21
                                                                                                                                            41
                                                                                                                                                                                                                                           178
                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CXSXPRXBXSXBXPXPXPXPXPXPXPXSXSXSXBXPXPXPXPX
                                        쉱
                                                                             8
                                                                                                     g
                                                                                                                                         ò
                                                                                                                                                                   g
                                                                                                                                                                                                    \delta
                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                           장염
                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune remember in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Pusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis mature Rais (N-terminus of MTB32A, RAisFL) antigen encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MI5 or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                                                                                                                                           Vaccine; immunity; diagnostic agent; gene therapy; Ra35 antigen; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1002 BP; 169 A; 331 C; 342 G; 160 T; 0 U; 0 Other;
                                                                                                                                                                               Mycobacterium tuberculosis mature Ra35 antigen encoding DNA
                                                                                                                                                                                                                                                                                         Location/Qualifiers
4. .996
7.tag= a /product= "Ra35 mature antigenic protein" /product= "Ra56" (pos:547. .549, aa:3ap) /transl_except= (pos:550. .552, aa:3er)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1002
128
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                   981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 79; 155pp; English.
Guderian
                                                                                  ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.856-54
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002WO-US008223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-2001; 2001US-0275837P
                                                                                  AAD47077 standard; DNA; 1002
                                                                                                                                                                                                                                                                Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky Y, Brannon M,
                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-759844/82.
P-PSDB; AAE29702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200272792-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-2002;
                                                                                                                                                 27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-2002
                                                                                                                AAD47077;
                     958
```

AADA 7077

XXX
XAAAA 7077

AADA 7

BP.

```
present invention relates to fusion proteins containing at least two
Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a
                                                                                                                      Disclosure, Page 95; 136pp; English.
                                                                                                                                                                                                    The
```

US-09-684-215B-23 (1-128) x AAD47077 (1-1002)

Query Match: DB:

aa:Asp) aa:Ser)

```
8888888888888888888888888
```

compositions comprising such fusion proteins. The present invention compositions compositions described that the particularly relates to nucleic acids encoding fusion proteins that include two or more individual Mitch increase the serological sensitivity of sera from individuals infected with include two or more individual mitched mitch increase the serological and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BoG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or call-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A full intradermal skin test. The present sequence is a cDNA encoding Mycobacterium species MTB32A (Ra32FL) mature protein Mycobacterium species antigens, nucleotides encoding them and

Sequence 1002 BP; 169 A; 331 C; 342 G; 160 T; 0 U; 0 Other;

1000 1200 000 000
Length: Matches: Conservative: Mismatches: Indels:
2.85e-54 651.00 100.00% 100.00% 6
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:

US-09-684-215B-23 (1-128) x AAD28336 (1-1002)

GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120 957 118 ATCGGCCTACCGCCTTCCTCGGCTTCGGTGTTGTTGTCGACAACGACGGCAACGGCGCACGA 777 80 1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProile 20 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal ThrGlyAsnValThrLeuAlaGlu 128 81 121 101 21 qq q ద g ద ò ò $\dot{\delta}$ ò à 셤 à g ò

Mycobacterium species Ra35FLMutSA mutant cDNA. AAD28337 standard; cDNA; 1002 (first entry) 22-APR-2002

Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; Ra32FLMutSA; mutant; mutein; ss.

The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual with tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with increase the serological sensitivity of sera from individuals infected with creatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BGC. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polymucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunicated for raising anti-M. tuberculosis and the patient and for raising anti-M. tuberculosis and in an animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents of the intradermal skin test. The present sequence is a oDNA encoding meanimm and manner also were also were also and the animal sequence is a consequence and the invention are useful as in vivo diagnostic agents and manner also were also an on-human animal sequence and the invention are useful as in vivo diagnostic agents and manner also were also and an animal contains and the present manner and only an encoding and an animal sequence proteins and the present manner and only an encoding and an animal sequence proteins and the present manner and only an encoding and an animal sequence proteins and the present manner and only Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject. Mycobacterium species Ra32FL mature protein mutant, Ra32FLMutSA Sequence 1002 BP; 169 A; 331 C; 341 G; 161 T; 0 U; 0 Other; /*tag= a /product= "Ra35FLMutSA protein" Claim 67; Page 96-97; 136pp; English. Location/Qualifiers Σ Skeiky Y, Reed S, Alderson 20-JUN-2001; 2001WO-US019959 20-JUN-2000; 2000US-00597796. 01-FEB-2001; 2001US-0265737P 966. (CORI-) CORIXA CORP. 2002-147798/19. Mycobacterium sp. P-PSDB; AAE17567 WO200198460-A2

1002 128 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: 2.85e-54 651.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: DB:

US-09-684-215B-23 (1-128) x AAD28337 (1-1002)

658 dedeckádedakádakátodokadakódakádatódagadagadatokódatódak 717 40 9 21 GlyGlnalaMetalaIleAlaGlyGlnIleArgSerGlyGlyGerProThrValHis 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGhealaileProile | IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 41 g ò g Š

909

80

100

849

729

20

789 9

40

61 778

ð g

ద

838 101 868 121

ò a ઠે g ð 원 AAX34251;

10

```
Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression.
                                                                                                                                                                                                                                                                                                                                                                                             101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                               910 ATCACCGCGTCGACGGCGCTCCGATCAACTCGGCCACGCGGATGGCGGGACGCGCTTAAC 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAX34001-X34252 represent nucleic acids encoding secreted proteins from various Mycobacterium species microorganisms. The nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for
                                                                                                                         BSO GICCAACGCGIGGETGGGAGGGGCICCGGCGAGAGTCTCGGCATCTCCACCGACGACGTG
                                                                                                                                                                                                                                                                                                                        IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
                                                                   570 Acedececerecearaacriceaerereceaeereeeereeeeaarreeearreeearre
                                                                                                                                                                             41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                  61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                  1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProIle
                                                                                                      21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guigueno A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium species nucleic acid sequence 50F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lim E, Pelicic V, Y;
US-09-684-215B-23 (1-128) x AAX34251 (1-1068)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1030 ACAGGGAACGTGACATTGGCCGAG 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Fig 50F; 309pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX34252 standard; DNA; 1143 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97FR-00010404
97FR-00011325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-FR001813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gicquel B, Portnoie D, Goguet De La Salmoniere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-181045/15.
P-PSDB; AAY04830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9909186-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-1997;
11-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1999
                                                                                                                                                                                                                                                                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX34252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                ठे
                                                                                                                                     요
                                                                                                                                                                             충
                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated
                                                                                                                                                                             GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                             81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                  ATCACCGCGCTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 897
 718 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCAACGGCGCACGA 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAX34001-X34252 represent nucleic acids encoding secreted proteins from various Mycobacterium species microorganisms. The nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection
                                    ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted protein, Mycobacterium, primer, PCR, amplification, probe, hybridisation, detection, vaccine, immunisation, infection, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1068 BP; 169 A; 352 C; 375 G; 172 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guigueno A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1068
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium species nucleic acid seguence 50D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pelicic V,
                                                                                                                                                                                                                                                      ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                          958 ACAGGGAACGTGACATTGGCCGAG 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 22; Fig 50D; 309pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gicquel B, Portnoie D, Lim E, Goguet De La Salmoniere Y,
                                                                                                                                                                                                                                                                                                                                                                  댎
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97FR-00010404.
97FR-00011325.
                                                                                                                                                                                                                                                                                                                                                                AAX34251 standard; DNA; 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.06e-54
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-181045/15.
P-PSDB; AAY05000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9909186-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-1997;
11-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1999
```

```
81 ileThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                   IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                      ValGInArgValValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspVal 80
                                                                                                                                                                ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= No start or stop codon. Although the sequence does contain an in frame stop codon, 2 further amino acids are shown in Figure 8 as being encoded by the present sequence, without a further stop codon"

25. 426
/*tag= b
/*note= "Region derived from TDRA12"
                                                                                                                           ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyPheAlaIleFroIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding antigen HTCC#1 fusion protein #4
                  395 G; 186 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .1629
7.tag= a
/product= "TDRA12-HTCC#1"
/prodlc= "TDRA12-HTCC#1"
/trand| except= (pos:1621. .1623, aa:Xaa)
/note= "Xaa= In frame STOP codon"
                                            1143
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TbRA12-HTCC#1, antigen, vaccine; tuberculosis; AIDS; acquired immunodeficiency disease; His Tag; ds.
                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
or viral
                                                                                                          (1-1143)
                                                                                                                                                                                                                                                                                                                                                   ThrGlyAsnValThrLeuAlaGlu 128
bacterial
                                                                                                            US-09-684-215B-23 (1-128) x AAX34252
                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                   ΰ
                                                                                                                                                                                                                                                                                                                                                                                                        AAS03793 standard; DNA; 1629
                   Sequence 1143 BP; 189 A; 373
                                           3.31e-54
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
 ø
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                             M. tuberculosis DNA
                                   Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                     1105
                                                                                                                                                                                                                                                                                               985
                                                                                                                             Н
                                                                                                                                              745
                                                                                                                                                                                                     41
                                                                                                                                                                                                                      865
                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                          925
                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                         AAS03793
                                                                                 Query Match
DB:
                                                                                                                                                                                                                                                                                                                                                                                     8 8
                                                                                                                                                                                                                                    8 B 8
                                                                                                                                                                                                                                                                                        원 상 원
                                                                                                                                                                                                                                                                                                                                                상
유
SXS
                                                                                                                                            Q
                                                                                                                                                            ò
                                                                                                                                                                               Dp
                                                                                                                              δ
```

```
144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                              The sequence encodes Mycobacterium tuberculosis fusion protein, TDRA12-HTCC#1 and includes a His tag at the N-terminus to aid purification. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 IleGlyProThrAlaPheLeuGlyJeuGlyValValBapAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyABpVal
205 GTCCAACGCGTGGGTCGGGGGTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 GlyHisHisFroGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä,
                                                                                                                                                                                                                                       Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens.
                                                                                                                                                                                            Lodes
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1629 BP; 298 A; 500 C; 535 G; 296 T; 0 U; 0 Other;
                                                                                                                                                                                            ö,
                                                                                                                                                                                            Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1629
128
0
0
0
/*tag= c
/note= "Region derived from Thrombin"
445. .1629
/*tag= "Region derived from HTCC#1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                            PD,
                                                                                                                                                                                             Reed S, Houghton RL, Mcneill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-215B-23 (1-128) x AAS03793 (1-1629)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                           Example 2; Fig 8; 168pp; English.
                                                                                                                2000WO-US028095.
                                                                                                                                     99US-0158338P.
99US-0158425P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 5e-54
651.00
100.00%
100.00%
                                                                                                                                                                                                                   WPI; 2001-290576/30.
                                                                                                                                                                        (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                    WO200124820-A1
                                                                                                                10-OCT-2000;
                                                                                                                                       07-OCT-1999;
07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                          misc feature
                                                                                           12-APR-2001
                                                                                                                                                                                               Skeiky Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                     . No. :
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
```

```
385 ACAGGGAACGTGACATTGGCCGAG 408
```

US-09-684-215B-23 (1-128) x AAL40771 (1-1742)

AAL40771 standard; DNA; 1742 BP

(first entry) 03-OCT-2002 AAL40771;

Nucleotide sequence encoding Ra12-WT1 fusion protein.

Ral2; serine protease antigen; WTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.

Unidentified Chimeric Location/Qualifiers
4. .1740
/*tag= a
/product= "Ra12-WT1 f

"Ral2-WT1 fusion protein"

WO200125401-A2

12-APR-2001

06-OCT-2000; 2000WO-US027652.

07-OCT-1999; 99US-0158585P.

(CORI-) CORIXA CORP.

Skeiky Y, Guderian J;

WPI; 2001-266299/27. P-PSDB; AAO22140.

Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.

Disclosure; Fig 4; 39pp; English

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polymucleotide sequence

Sequence 1742 BP; 372 A; 569 C; 490 G; 311 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 5.46-54 651.00 100.00% 100.00% Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.:

144 100 324 384 204 264 9 80 84 40 20 81 ileThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 265 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGTTAAC 25 ACGGCCGCGTCCGATAACTICCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCGATC 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 145 ATCGGGCCTACCGCTTCCTCGGCTTGGGTGTTGTCGACAACGACAACGGCGCACGA 205 GrccaAcGcGrcGrcGGGAGCGCrcCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGT ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 385 ACAGGGAACGIGACATIGGCCGAG 408 121 ThrGlyAsnValThrLeuAlaGlu 128 н 셤 8 d g 8 g ઠે 셤 ò 8

AAL40768 standard; DNA; 1871 BP

AAL40768;

03-OCT-2002 (first entry)

Nucleotide sequence encoding MTB32A protein.

Ral2; serine protease antigen; WTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.

Mycobacterium tuberculosis.

Location/Qualifiers 89. .1156 /*tag= a

/product= "Bacillus mycobacterium MTB32A protein"

WO200125401-A2

12-APR-2001.

06-OCT-2000; 2000WO-US027652

99US-0158585P 07-OCT-1999;

(CORI-) CORIXA CORP

Skeiky Y, Guderian J;

WPI; 2001-266299/27. P-PSDB; AAO22137.

Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.

Disclosure, Fig 1, 39pp, English.

The invention relates to a recombinant nucleic acid molecule encoding

tusion polypeptide, comprising a polymucleotide sequence of Ral2, a 14

KDB C-terminal fragment of serine protease antigen MTB32A of
Mycobacterium tubercuiosis, and a heterologous polymucleotide sequence.
The recombinant fusion nucleic acids and polypeptides are useful for
providing stable and high yield expression of fusion polypeptides of both
cukaryotic and prokaryotic origin and to encode a protein product for use
as an antigen for detecting serum antibodies. The presence of serum
antibodies to M. tuberculosis antigens in an individual indicates that
the individual is infected with it. The fusion polypeptides are useful as
cources of proteins for monitoring binding of serum antibodies to fusion
proteins and as an immunogen to induce and/or enhance immune responses.
The coding sequences can be ligated with a coding sequence of another
molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and
can be used in vivo as a DNA vaccine. This polymucleotide sequence
cerves of protein the DNA encoding the Mycobacterium tuberculosis MTB32A protein 8 \times 9 \times 9

Sequence 1871 BP; 317 A; 617 C; 605 G; 332 T; 0 U; 0 Other;

21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40 938 GTCCAACGCGTGGTCGGAAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 878 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGCCAACGCGCACAA 998 ATCACCGCGGTCCACCGGCGCTCCGATCAACTCCGCCACCGCGATGGCCGACGCGCTTAAC 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 1871 128 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-684-215B-23 (1-128) x AAL40768 (1-1871) 5.87e-54 651.00 100.00% 100.00% Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.: Score: 81 g g à ò g QQ g ઠ δ à qq ò

877

937

9

1118 ACAGGGAACGTGACATTGGCCGAG 1141 ThrGlyAsnValThrLeuAlaGlu 128 121 ð g

ADA26353 standard; DNA; 2181 BP

ADA26353;

20-NOV-2003 (first entry)

b; fusion polypeptide; MTB32A; MTB39; antigen; MTB32A; MTB39; tuberculosis; tuberculostatic; gene therapy; vaccine. gene; fusion MTB85A; ds;

Mycobacterium MTB32-MTB39F fusion protein encoding DNA.

Mycobacterium sp.

ThrGlyAsnValThrLeuAlaGlu 128

121

à

```
/*tag= a
/product= "MTB32-MTB39F fusion polypeptide"
.2175
SOC
FFFXHXCXFXHXXHXHHXHXHXHXHXSXXCCCCCCXX
```

WO2003070187-A2

28-AUG-2003

15-FEB-2002; 2002US-0357351P.

18-FEB-2003; 2003WO-US004903.

(CORI-) CORIXA CORP

Reed Skeiky Y, Guderian J,

ŝ

New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection. WPI; 2003-697554/66. P-PSDB; ADA26354.

Claim 1; Fig 1; 112pp; English.

The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen; or WTB32A, WTB39 and MTB85A antigen from a Mycobacterium species of the uberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a polynucelotide of the invention may have a use in gene therapy, and as a vectine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.

Sequence 2181 BP; 341 A; 693 C; 792 G; 355 T; 0 U; 0 Other;

US-09-684-215B-23 (1-128) x ADA26353 (1-2181)

1057

997

80

1117

100 838 ATCACCGCGCGCCCGGCGCTCCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 897 120 717 777 837 957 657 9 80 40 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGerProThrValHis 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 718 Arcadactraccactrecreagerregererrereacaacaacaacaacaacaacaacaa ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 81 11eThralavalaspGlyalaProlleAenSeralaThralaMetAlaAspAlaLeuAsn 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaileProl . 19 658 778 101 868 d g g g g ద ઠે à 8 8 8 ઠે

us-09-684-215D-23.rud

958 ACAGGGAACGTGACATTGGCCGAG 981

JS-09-684-215B-23 (1-128) x AAD47084 (1-2190)

AAD47084 standard; DNA; 2190 RESULT 16 AAD47084

AAD47084;

(revised)
(first entry) 29-AUG-2003 27-JAN-2003 Mycobacterium sp. MTB72FMutSA fusion protein encoding DNA

Vaccine, immunity, diagnostic agent, gene therapy, TbH9, antigen, Ra35MutSA, Ra12, MTB72MutSA, chimeric, gene; ds.

Mycobacterium sp. Mycobacterium tuberculosis.

Location/Qualifiers 1. .2190 /*tag= a /product= "MTB72FMutSA fusion protein"

WO200272792-A2

19-SEP-2002

13-MAR-2002; 2002WO-US008223

13-MAR-2001; 2001US-0275837P

(CORI-) CORIXA CORP

Guderian J; Skeiky Y, Brannon M,

WPI; 2002-759844/82. P-PSDB; AAE29709.

New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium

Disclosure; Page 92-93; 155pp; English.

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polypeptide sequence encoding an antigen or an antigenic fragment from polypeptide or its fragment. The Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, Leff, MIS, and 6H polymucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is a nimal. The invention is used in gene therapy. The present sequence is a nimal protein and Ralz protein from M. tuberculosis and TDH9. Protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS field)

Sequence 2190 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 0 Other;

/*tag= d /note= "Ra35 DNA fragment" replace(2128, T) /*tag= e

WO200198460-A2

27-DEC-2001

1603. .2187

misc_feature

mutation

misc_feature

misc_feature

21190 128 0 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 7.05e-54 651.00 100.00% 100.00% 100.00% Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.:

20-JUN-2000; 2000US-00597796. 01-PEB-2001; 2001US-0265737P. 20-JUN-2001; 2001WO-US019959

(CORI-) CORIXA CORP

81 ileThralaValaspGlyAlaProileAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100 101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120 141 201 261 321 40 9 80 20 81 22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCGATC 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProlle ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB72FMutSA; Ra12-TbH9-Ra35MutSA; mutant; mutein; ds. Mycobacterium species MTB72FMutSA fusion protein encoding DNA. Location/Qualifiers
1. .2190
7.tag= a /product= "MTB72FMutSA fusion protein"
22. .417
/*tag= b /mote= "Ral2 DNA fragment"
424. .1596
/*tag= c /mote= "TPH9FL DNA fragment" 382 ACAGGGAACGIGACATIGGCCGAG 405 ThrGlyAsnValThrLeuAlaGlu 128 AAD28343 standard; DNA; 2190 BP 22-APR-2002 (first entry) Mycobacterium sp. 121 61 AAD28343; RESULT 17 AAD28343

IID AAD2

XX AAD2

XX AAD2

XX AAD2

XX AAD2

XX X AAD2

XX X W FUB II

XX X W IUDE

XX X W IUDE

XX X III

YOUR II

YOUR III

YOUR II

YOUR III

YOUR III 셤 원 요 ઠ 셤 8 셤 ઠે 셤 ò à

```
3 06:36:18 2004
```

Skeiky Y, Reed S, Alderson M;

2002-147798/19 P-PSDB; AAE17573 Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject

Claim 81; Page 108-109; 136pp; English.

Mycobacterium species antigens, nucleotides encoding them and comprising such fuaion proteins. The present invention particularly relates to nucleic acids encoding them and particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the exployactal sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BGG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium infection. The fusion proteins and the autibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as antibodies or cell-mediated immunity against M. tuberculosis, for the patient and for raising anti-M. tuberculosis antibodies in a non-human operator of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a DNA encoding manning means to be accoming means and for raising and means an

Sequence 2190 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 0 Other;

2190 128 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 7.05e-54 651.00 100.00% 100.00% Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:

US-09-684-215B-23 (1-128) x AAD28343 (1-2190)

	382 ACAGGGAACGTGACATTGGCCGAG 405	385	g
	ThrGlyAsnValThrLeuAlaGlu 128	121	à
381	GGGCATCATCCCGGTGATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT	322	g
120	GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg	101	ò
321	ATCACCGCGCTCGACGCGCTCCGATCGACTCGGCCACCGCGATGGCGGACGCGCTTAAC	262	Db
100	IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn	81	ò
261	GTCCAACGCGTGGTCGGGAGCGCTTCCGGCGGCAAGTCTCGGCATCTCCACGGGGGACGTG	202	qq
80	ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal	19	ò
201	ATCGGGCCTACCGCCTTCCTCGGCTTGGTTGTTGTCGACAACAACGGCAACGGCGCACGA	142	Д
9	IleGlyProThrhlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg	41	à
141	GGGCAGGCGATGGCGATCGGGGCCAGATCCGATCGGGTGGGGGGGCACCCCACCGTTCAT	82	g
40	GlyGlnAlaMetAlalleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis	21	ò
81	ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCATTC	22	d d
20	ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle	-	ò

ВЪ. AAL40773 standard; DNA; 2191

AAL40773;

(first entry) 03-OCT-2002

Nucleotide sequence encoding Ral2-H9-32A fusion protein.

Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.

Unidentified.

Chimeric

Location/Qualifiers 1. .2190 /*tag= a /product= "Ral2-H9-32A fusion protein"

WO200125401-A2

12-APR-2001

06-OCT-2000; 2000WO-US027652.

99US-0158585P. 07-OCT-1999;

(CORI-) CORIXA CORP.

Skeiky Y, Guderian J;

WPI; 2001-266299/27. P-PSDB; AAO22142.

Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.

Disclosure, Fig 6; 39pp; English.

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 (busion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 (busion polypeptide) and a beterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The odding sequence con a individual sequence con a nother molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence represents the DNA encoding the Ra12-H9-32A fusion protein

Sequence 2191 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 1 Other;

Pred. No.:	7.05e-54	Length:	2191
	651.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Ouery Match:	100.00%	Indels:	0
ĎB:	4,	Gaps:	0

US-09-684-215B-23 (1-128) x AAL40773 (1-2191)

```
42. .2231

*tag= a
/product= "Mtb32-Mtb39"
/transl_except= (pos:498. .506, aa:Asn-Ala)
/transl_except= (pos:597. .605, aa:Ala-Gln)
/transl_except= (pos:597. .605, aa:Ala-Gln)
/transl_except= (pos:998. .802, aa:Ala)
/note= "This codon has an apparent 2 nucleotide insertion
which alters the reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                   ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCGACGA 201
                                                                                                                                                                                                                                                                                     GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 261
                                                                                                                                                                                                                                                                                                                                                      IleThralaValaspGlyAlaProlleAsnSerAlaThralaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGerProThrValHis 40
                                                                                                                                                       | IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                            80
ACGCCCCCCTCCGATAACTTCCCACTGTCCCAGGTGGCCAGGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                         ValGinArgValValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion protein; tuberculosis; Mycobacterium tuberculosis; gene; ds;
tuberculostatic; immunogen; vaccine; Mtb32-Mtb39; Ra12; TbH9; Ra35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding antigenic fusion protein Ral2-TbH9-Ra35 (Mtb32-Mtb39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 42. .2231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-00818112.
97US-00942578.
98US-00025197.
98US-00056556.
98US-00223040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK14128 standard; DNA; 2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00287849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REED S G.
SKEIKY Y A.
DILLON D C.
ALDERSON M.
CAMPOS-NETO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002009459-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ra12-TbH9-Ra35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-1997;
01-OCT-1997;
18-FEB-1998;
07-APR-1998;
30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2003
08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-2002
                                                                                                                                                            41
               22
                                                                21
                                                                                                                 82
                                                                                                                                                                                                             142
                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                       202
                                                                                                                                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                         262
                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK14128,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REED/)
(SKEI/)
(DILL/)
(ALDE/)
(CAMP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK14128

XX

AX

AX

ABK1

XX

ABK1

XX

ABK1

XX

ABK1

XX

XX

ABK1

XX

ABK1

XX

ABK1

XX

ABK1

XX

ABK1

XX

ABK1

XX

ABC1

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
       셤
                                                                8 8 8
                                                                                                                                                                                                 6
6
                                                                                                                                                                                                                                                                                                요
                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

07.00.00

h

HOII MAY

```
The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are particularly to diagnosing, treating or peventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents DNA encoding an M. tuberculosis fusion protein of the invention. (Updated on 29-AUG-2003 to standardise of field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 IleThrhlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValGlnargValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ThralaalaSeraspasnPheGInLeuSerGlnGlyGlyGlnGlyPhealaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 IleGlyProThrAlaPheLeuGlyLeuGlyValValValAspAsnAsnGlyAsnGlyAlaArg
                                                                           useful
                                                                           New fusion proteins of Mycobacterium tuberculosis antigens, usef diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.
           Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis antigen fusion protein Mtb32A DNA.
           Campos-Neto
                                                                                                                                                                                                                                                                                                                       Seguence 2286 BP; 373 A; 719 C; 807 G; 381 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                              758
758
000
000
000
                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
          Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-23 (1-128) x ABK14128 (1-2286)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGGGAACGTGACATTGGCCGAG
            Dillon DC,
                                                                                                                                 Example; Fig 1; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ20194 standard; DNA; 2287
                                                                                                                                                                                                                                                                                                                                                          7.41e-54
651.00
100.00%
100.00%
            Skeiky YA,
                                     WPI; 2002-171134/22,
P-PSDB; AAU74588.
                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-2000
              SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ20194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 20
AAZ20194
ID AAZ20.
XX
AC AAZ20.
XX
DT 17-JA:
XX
DE Mycob
              Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
8 8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 6 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \dot{\delta}
```

3 Ub:35:18 2004 Mon May

Tuberculosis, antigen; fusion protein; Mtb32A; Ra12; TbH9; Ra35; diagnosis; therapy; vaccine; immunogen; ss. Skeiky YAW, Alderson M, Campos-Neto A; Location/Qualifiers 42. .2231 /*tag= a 99WO-US007717 98US-00056556. Mycobacterium tuberculosis. WPI; 1999-601610/51. P-PSDB; AAY32059. (CORI-) CORIXA CORP. 07-APR-1998; 30-DEC-1998; 07-APR-1999; W09951748-A2 14-OCT-1999.

GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120

101

363 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAACTCGGGCACGGCACGT

ઠ 셤

422

New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis.

Example, Fig 1A-B, 83pp; English.

This DNA sequence includes a coding region for a recombinant (See AAY32059), Mycobacterium tuberculosis tri-antigen fusion protein (See AAY32059), termed Mtb322A, composed of the antigens Rai2, TBH9 and Rai3. The DNA is useful for the recombinant production of the fusion protein. Coding sequences for the antigens were modified by PCR in order to facilitate their tusion and subsequent expression of the fusion protein. 3 Coding sequences for Rai2, TBH9 and Rai2 were ligated to encode Mtb32A. The invention provides fusion proteins (see AAY32059-71) containing at least invention provides fusion proteins and polymucleotides encoding them are useful as vaccines for preventing tuberculosis encoding them are useful as vaccines for preventing tuberculosis (laimed), for disposis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein components

Sequence 2287 BP; 374 A; 723 C; 805 G; 382 T; 0 U; 3 Other;

21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40 2287 128 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-09-684-215B-23 (1-128) x AAZ20194 (1-2287) 7.41e-54 651.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: DB: à d ò g

ValGlnargValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80

61

ò g

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous fusion polypeptide sequence encoding an antiège nor an antiègenic fragment from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, LeIF, MIS, and 6H polymucleotides. Sequence encoding a care used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion propetides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human and mannel. The invention is used in gene therapy. The present sequence is a nimal. The invention protein. This fusion protein comprises Ralz and Rals protein from Mycobacterium tuberculosis and TDH9 protein from Mycobacterium tuberculosis and TDH9 protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS field) New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynuclectide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis. Vaccine, immunity, diagnostic agent; gene therapy, TbH9, antigen, Ra35; Ra12; WTB72F; chimeric; gene; ds. Mycobacterium sp. MTB72F fusion protein encoding DNA. Location/Qualifiers 42. 2231 /*tag / /product= "MTB72F fusion protein" Disclosure, Page 87-90, 155pp, English. Guderian J; 13-MAR-2002; 2002WO-US008223. 13-MAR-2001; 2001US-0275837P. AAD47083 standard; DNA; 2287 Mycobacterium sp. Mycobacterium tuberculosis. Chimeric. 29-AUG-2003 (revised) 27-JAN-2003 (first entry) Skeiky Y, Brannon M, WPI; 2002-759844/82. P-PSDB; AAE29708. (CORI-) CORIXA CORP WO200272792-A2 19-SEP-2002 AAD47083; AAD47083
AAD47083
XX
AAD47083
XX
AAD47083
DT 29-AU
DT 27-UA
DT 27-UA
DT 27-UA
DT 29-AU
DT 27-UA
COS Mycob

```
Alignment Scores:
셤
                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                염
                                                                                                                                                                                                                                                                                                                                                                                           ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                    ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                            IleThralavalaspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                   GTCCAACGCGTGGGAGGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 302
                                                                                                           20
                                                                                                     40
                                                                                                                                                    ValGinArgValValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspVal 80
                                                                                                   GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                    63 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                            ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProIle
                                                                                                                                                                                                                                                                                                                 Fusion protein, antigen, serological sensitivity, immune response, tuberculosis; infection, vaccine; MTB72F; Ra12-TbH9-Ra35; ds.
    Sequence 2287 BP; 372 A; 717 C; 814 G; 381 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                     Mycobacterium species MTB72F fusion protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                US-09-684-215B-23 (1-128) x AAD47083 (1-2287)
                                                                                                                                                                                                                             ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                   ACAGGGAACGTGACATTGGCCGAG 446
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                AAD28342 standard; DNA; 2287 BP
                      7.41e-54
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                        22-APR-2002 (first entry)
                           Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                   Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200198460-A2
                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                               27-DEC-2001
                                                                            Н
                                                                                                     21
                                                                                                                                                    61
                                                                                                                                                                243
                                                                                                                                                                            81
                                                                                                                                                                                        303
                                                                                                                                                                                                    101
                                                                                                                                                                                                                363
                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                       423
                                                                                                                                                                                                                                                    à
                                                                                       g
                                                                                                     ò
                                                                                                              d
                                                                                                                           ઇ
                                                                                                                                        셤
                                                                                                                                                              CD
                                                                                                                                                                            \stackrel{>}{\circ}
                                                                                                                                                                                      셤
                                                                                                                                                                                                   ò
                                                                                                                                                                                                               a
                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                      a
                                                                                                                                                  ∂
```

```
The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infection the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polymucleotides are useful as diagnostic tools in partients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or call-mediated immunity against M. tuberculosis, for the invention or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A animal sequences of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a DNA encoding Mycobacterium species MTB32F (Ral2-TDH9-Ral35) fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                       Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 IleGlyProThrAlaPheLeuGlyLeuGlyValValBapAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 GGCAGGCGATGGCGATCGCGGCCAGATCGGGTGGGGTGACCCATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2287 BP; 372 A; 717 C; 814 G; 381 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2287
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215B-23 (1-128) x AAD28342 (1-2287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 62; Page 103-106; 136pp; English.
                                                                                                                                                                                                                           Ξ
                                                                                                                                                                                                                           Skeiky Y, Reed S, Alderson
                                                       20-JUN-2000; 2000US-00597796.
01-FEB-2001; 2001US-0265737P.
20-JUN-2001; 2001WO-US019959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.41e-54
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                      WPI; 2002-147798/19
P-PSDB; AAE17572.
                                                                                                                                                         (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
```

122

182

242

100

324

264

205 GTCCAACGCGTGGTGGTGCGCTCCGGCGCAAGTCTCGGCATCTCCACCACGAGGTGTG

ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal

61

à ద 8

265 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 325 GGGATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCA

셤 ઠે ద 8

셤

ADA26359 standard; DNA; 2487

81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn

80

204

9

40

GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis

21

원 8 a 8 8

145 ATCGGGCCTACCGCCTTCCTCGCTTGGGTGTTGTCGACAACAACGGCAACGGCACGA

41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg

25 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 84

120

384

```
The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB32B and MTB85A antigen. From a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculosia; tuberculosia;

    4. .2445
    /*tag= a
    /product= " MTB72F-DPV (fusion MTB81F) protein"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium MTB72F-DPV (fusion MTB81F) protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2451 BP; 389 A; 785 C; 870 G; 407 T; 0 U; 0 Other;
                                                                                                                                                  ThrglyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 84; Fig 8; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-2003; 2003WO-US004903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-FEB-2002; 2002US-0357351P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA26360 standard; DNA; 2451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guderian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-697554/66.
P-PSDB; ADA26367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric.
Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003070187-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky Y,
                                                           363
                                                                                                                                                            121
                                                                                                                                                                                                                                                        423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA26360;
                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                          ADA26360

IID ADA2

ANX
ANX
ANX
ADA2

XXX
ADA2

XXX
ADA2

XXX
ADA3

XXX
ADA3

XXX
ADA3

ADA3

ADA4

ADA5

AD
                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                           g
                                                                                                                                                                                                                                        g
                                                                                                                                                       ઠે
```

ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculosi; tuberculosis; tuberculosis; tuberculosis; tuberculosis; tuberculosis; tuberculosis; tuberculosis; tuberculosis; tuberculosis;

Mycobacterium sp.

Chimeric

WO2003070187-A2

Mycobacterium MTB72F-MTI (fusion MTB83F) protein encoding DNA

(first entry)

20-NOV-2003

ADA26359;

Location/Qualifiers
4. .2481
4. frage a "MTB72F-MTI (fusion MTB83F) protein" /product = "MTB72F-MTI (fusion MTB83F)

```
The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTB92A and integen, or MTB32A, MTB39 and MTB82A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A
                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 84; Fig 7; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                   Reed S;
                                                                                                                                                                                                                                                                                                        LS-FEB-2002; 2002US-0357351P.
                                                                                                                                                                                                                                                                                  18-FEB-2003; 2003WO-US004903
                                                                                                                                                                                                                                                                                                                                                   Skeiky Y, Guderian J,
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-697554/66.
P-PSDB; ADA26366.
                                                                                                                                                                                                                                                                                                                              CORP
                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA
                                                                                                                                                                                                                                                            28-AUG-2003
```

20

1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlyPheAlaIleProIle

(1-2451)

US-09-684-215B-23 (1-128) x ADA26360

2451 128 0 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

8.03e-54 651.00 100.00% 100.00%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores: Pred. No.:

```
3 06:36:18 2004
```

18-02-684-712D-73

145 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCACGACGCACGA 204 81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100 265 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 324 polynucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention. 264 IleGlyProThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80 ds, gene, fusion protein, MTB32A, MTB39, antigen, MTB32A, MTB39, MTB85A, tuberculosis, tuberculostatic, gene therapy; vaccine. 205 GICCAACGCGTGGTCGCGAGCGCTCCGGCGGCGCAAGTCTCCGGCATCTCCACCGGCGACGTG ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProIle Mycobacterium MTB72F-Erd14 (fusion MTB89F) protein encoding DNA Sequence 2487 BP; 394 A; 784 C; 896 G; 413 T; 0 U; 0 Other; Location/Qualifiers
4.2631
4.tag= //tag= "MTB72F-Erd14 (fusion MTB89F)" 2487 128 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: (1-2487)ThrGlyAsnValThrLeuAlaGlu 128 385 ACAGGGAACGTGACATTGGCCGAG 408 US-09-684-215B-23 (1-128) x ADA26359 ADA26358 standard; DNA; 2637 BP 18-FEB-2003; 2003WO-US004903 B.17e-54 651.00 100.00% 100.00% (first entry) Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: gb. WO2003070187-A2 Chimeric. Mycobacterium Alignment Scores: Pred. No.: 20-NOV-2003 28-AUG-2003 121 ADA26358; 41 RESULT 25
ADA26358
XX
AC ADA26
XX
XX
DT 20-NO
DT 20-NO
DX
XX
XX
Chime
OS Mycob
XX
Chime
CS Mycob
XX
Chime
XX
Ch 8 6 ò g 8886666 qq 8 B S g à 셤 ò g ò

15-FEB-2002; 2002US-0357351P

The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB32A, MTB35A and MTB35A antigen, or MTB32A, MTB35A and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention. 81 ileThrAlaValAspGlyAlaProileAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100 101 GlyhishisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120 264 324 384 20 84 80 New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB33 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection. edecarcarcecegreacercarerecegreacerescaaaceaaercesecegereser ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGTTAAC 61 ValGinArgValValGiySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAepVal 1 ThralaalaserAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle Seguence 2637 BP; 428 A; 840 C; 928 G; 441 T; 0 U; 0 Other; 2637 128 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-09-684-215B-23 (1-128) x ADA26358 (1-2637) Claim 84; Fig 6; 112pp; English. ŝ AAD47110 standard; DNA; 2808 Reed 8.74e-54 651.00 100.00% 100.00% 100.00% (revised)
(first entry) **ب** Guderian WPI; 2003-697554/66. P-PSDB; ADA26365. CORI-) CORIXA CORP Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: 29-AUG-2003 27-JAN-2003 ,, 265 325 121 AAD47110 Skeiky AAD47110 ID AAD47110 XX AAC AAD47 XX DT 29-AU DT 27-JA B g ò g 8 8 8 g 요 ð ò 8 8

/product= "Mycobacterium sp. MTB72F-Leishmania sp. MAPS (aka r95f) fusion protein" Mycobacterium sp. MTB72F-Leishmania sp. MAPS (aka r95f)-fusion DNA. Vaccine, immunity, diagnostic agent; gene therapy, MTB72F; MAPS; chimeric; gene; ds. Location/Qualifiers
4. .2796
/*tag= a
/product= "Mycobacter Guderian J; 13-MAR-2001; 2001US-0275837P. Skeiky Y, Brannon M, (CORI-) CORIXA CORP. Mycobacterium sp. WO200272792-A2 Leishmania sp. Chimeric. 13-MAR-2002; 19-SEP-2002

WPI; 2002-759844/82. P-PSDB; AAE29731.

New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MalS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.

Example 6; Page 128-129; 155pp; English

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from molecular spiral and a Laishmania polynucleotide sequence encoding a polyneptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to eliciting protective immunity against pathogenic polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for ration and mycobacterium sp. witholdes in a non-human or mimal. The invention is used in gene therapy. The present sequence is mycobacterium sp. WTB72F (ax 195f) fusion DNA, This sequence comprises Mycobacterium sp. MTB72F (ax 195f) fusion DNA, This sequence comprises Mycobacterium sp. MTB72F (ax 195f) fusion DNA, This sequence comprises Mycobacterium sp. MTB72F (ax 195f) fusion DNA, This sequence comprises Mycobacterium sp. MTB72F (ax 195f) fusion DNA, This sequence comprises Mycobacterium sp. MTB72F (ax 195f) fusion COMPSE standardise OS field)

Sequence 2808 BP; 466 A; 889 C; 982 G; 471 T; 0 U; 0 Other;

2808 128 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 9.48-54 651.00 100.00% 100.00% 100.00% Similarity: Percent Similarity: Best Local Si Query Match: DB:

US-09-684-215B-23 (1-128) x AAD47110 (1-2808)

- 84 25 ACGGCCGCGTCCGATAACTTCCGAGTCCCAGGGTGGGCAGGGATCGCCATTCCGATC 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle d ò
- 40 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis

100 324 384 204 264 144 80 9 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 265 AICACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 145 Arcadeceraccidectredectredergregicaecaacaacaacaacaacaacaaca 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 205 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGAGCGTG IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 121 ThrGlyAsnValThrLeuAlaGlu 128 385 ACAGGGAACGTGACATTGGCCGAG 408 41 82 a ò g 8 셤 à 셤 ò ઠે ద

RESULT 27

ADA26357 standard; DNA; 2808

ADA26357;

20-NOV-2003 (first entry)

Mycobacterium MTB72F-MAPS (fusion r95F) protein encoding DNA.

ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculostatic; gene therapy; Vaccine.

Mycobacterium sp. Chimeric

Location/Qualifiers
4. 2796
4. 4796
/*tag= a "MTB72F-MAPS (fusion r95F)"

WO2003070187-A2.

28-AUG-2003

18-FEB-2003; 2003WO-US004903

15-FEB-2002; 2002US-0357351P.

(CORI-) CORIXA CORP

Skeiky Y, Guderian J,

Reed S;

WPI; 2003-697554/66. P-PSDB; ADA26364.

New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.

Disclosure, Fig 5; 112pp; English.

The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB12A and MTB39 antigen, or WTB12A, MTB13B, and WTB85A, antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polynucelotide of the invention may have a use in gene therapy, and as a polynucelotide of the invention may have a the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.

ŝ

```
Reed
٦,
Guderian
              WPI; 2003-697554/66.
P-PSDB; ADA26356.
                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-2003
Skeiky Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                         Н
                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA26363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                  ò
à
                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                    ठ
                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                          GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                           145 ATCGGGCCTACCGCCTTCCTCGGCTTGTTGTTGTCGACAACAAGGCAACGGCGCACGG 204
                                                                                                                                                                                                       205 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGAACGT 264
                                                                                                                                                                                                                            81 IleThralaValaspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                           324
                                                                                                                                                                                                                                                                          384
                                                                                                                                                                                             80
                                                                                                 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                               41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                   ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                                                                                                             ValGlnArgValValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspVal
                                                                                                                                                                                                                                     325 GGGCATCATCCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAAGTCGGGGGGCACGGT
       U; 0 Other;
                              2808
1128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "MTB-120F fusion protein"
/note= "No stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium MTB-102F fusion protein encoding DNA
                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
         0
         ..
H
         471
                                                                                    (1-2808)
         982 G;
                                                                                                                                                                                                                                                                                                    385 ACAGGGAACGTGACATTGGCCGAG 408
                                                                                                                                                                                                                                                                                          ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1, .3030
/*tag= a
/product= "MTB-120F f
                                                                                    US-09-684-215B-23 (1-128) x ADA26357
                                                                                                                                                                                                                                                                                                                                        ADA26355 standard; DNA; 3030 BP
         ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-FEB-2002; 2002US-0357351P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-2003; 2003WO-US004903
         466 A; 889
                              9.46-54
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP
                       Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium sp.
         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003070187-A2
         Sequence 2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-2003
                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                              61
                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                        ADA26355
                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric
                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                         RESULT 28
                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                           8
                                                                                                                                                                                                            d
                                                                                                                                                                                                                             ò
                                                                                                   ठे
                                                                                                                 d
                                                                                                                                 ઠ્ઠ
                                                                                                                                              g
                                                                                                                                                               à
                                                                                                                                                                            g
```

```
The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB12A and MTB39 antigen, or MTB12A, MTB12A and MTB39 antigen, or MTB12A, MTB13B, MTB18B3A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a vecture. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTB85A;
New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infectios.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                775 greeaacgegragreggeggaggereeggaggagrereggarereggareeggagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              səs Aceeccecerceanaacırceaecrerceaeereescaecaeaarreecarreear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           715 ArcesecciAcceccrrccrceecrresererrerceAcaacaaceaccaacecea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds, gene, fusion protein, MTB32A; MTB39, antigen, MTB32A; MTB39, N
tuberculosis; tuberculostatic, gene therapy; vaccine, MTB72F; 85B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. bovis MTB72F and 85b complex antigen (fusion MTB103F) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3030 BP; 498 A; 966 C; 1062 G; 504 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3030
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-684-215B-23 (1-128) x ADA26355 (1-3030)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВЪ
                                                                                                                                      Claim 5; Fig 3; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA26363 standard; DNA; 3060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.03e-53
651.00
100.00%
100.00%
```

```
The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB12A and MTB39 antigen, or MTB32A. MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a polynucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculosiatic; gene therapy; vaccine.
325 GGGATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "MTB72F-hTCC#1 (fusion MTB102tm2F) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium MTB72F-hTCC#1 (fusion MTB102tm2F) protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-684-215B-23 (1-128) x ADA26362 (1-3104)
                                                                                                                  385 ACAGGGAACGTGACATTGGCCGAG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
4. .3072
/*tag= a
                                                                                             121 ThrGlyAsnValThrLeuAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 84; Fig 10; 112pp; English
                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-FEB-2002; 2002US-0357351P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.06e-53
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                  ADA26362 standard; DNA; 3104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-2003; 2003WO-US004903
                                                                                                                                                                                                                                                                                                                                                                               20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky Y, Guderian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-697554/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ADA26369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003070187-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-AUG-2003
                                                                                                                                                                                                                                                                                                                            ADA26362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                         RESULT 30
                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB32A, MTB35A and MTB85A antigen. From a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymeclotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antiquens, with or without the MTB83A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyGlnalaMetAla1leAlaGlyGln1leArgSerGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGGGGCCTACCGCCTTCCTCGGCTTTGTCGACAACAACAACGGCAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrClyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                    /*tag= a /*tag= a //tag= a //t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3060 BP; 503 A; 977 C; 1070 G; 510 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3060
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1-3060)
                                                                                                                        Location/Qualifiers
4. .3054
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 84; Fig 11; 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-684-215B-23 (1-128) x ADA26363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score: 1.04e-53
Score: 651.00
Percent Similarity: 100.00%
Query Match: 100.00%
DB:
                                                                                                                                                                                                                                                                                                                                                                                     2003WO-US004903
                                                                                                                                                                                                                                                                                                                                                                                                                                        15-FEB-2002; 2002US-0357351P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guderian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-697554/66.
P-PSDB; ADA26370.
                                             Chimeric.
Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                        WO2003070187-A2
                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                               28-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
```

ò 셤 à 유 ò d 8 셤 ठ g ठे

```
20
                                                                                                                                      ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
Sequence 3104 BP; 510 A; 968 C; 1104 G; 522 T; 0 U; 0 Other;
                                  3104
128
0
0
                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
```

```
81 IleThralaValAspGlyAlaProIleAsnSerAlaThralaMetalaAspAlaLeuAsn 100
                                                                                                                                                                                                                              265 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 324
                                                                                                                                                                                                                                                                    101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                    85 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGGTCACCCCACCGTTCAT 144
                                                                                                           145 ATCGGGCCTACCGCCTTCCTCGGCTTCGGGTGTTGTCGACAACAACAACGGCAACGGCGCACGA 204
                            21 GlyGlnhlaMethlailehlaGlyGlnilehrgSerGlyGlyGerProThrValHis 40
                                                                                     41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAspAspAspGlyAsnGlyAlaArg 60
25 ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 84
                                                                                                                                                                                                                                                                                                                             121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                        385 ACAGGGAACGTGACATTGGCCGAG 408
                                                                          8 6 8 6 8 6
                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                       Dp
                      \delta
                                                  g
```

Search completed: April 29, 2004, 23:03:15 Job time : 368.096 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

									0 14		RESULT 1 US-09-287-849 Sequence 27 Sequence 27 GENERAL INF APPLICANT: APP	CURRENT APPL CURRENT FI PRIOR APPL PRIOR FILI	PRIOR APPL ; PRIOR FILI ; PRIOR PILI	, PRIOR FII
Gencore Version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - nucleic search, using frame plus p2n model	Run on: April 29, 2004, 22:43:07; Search time 469.129 Seconds (without alignments) 1234.209 Million cell updates/sec	Title: US-09-684-215B-23 Perfect score: 651 Sequence: 1 TAASDNFQLSQGQGFAIPISVTWQTKSGGTRTGNVTLAE 128	Scoring table: BLOSUM62 Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Ygapop 6.0 , Ygapext 7.0 Delop 6.0 , Delext 7.0	Searched: 2936184 segs, 2261732022 residues	Total number of hits satisfying chosen parameters: 5872368	Minimum DB seg length: 0 Maximum DB seg length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Command line parameters: -MODEL=frame+ p2n.model -DEV=xlh -Q=COGN2_1VGPTO spool/USDS084215/runat_29042004_061306_13266/app_query.fasta_1.1180 -Q=COGN2_1VGPTO spool/USDS084215/runat_29042004_061306_13266/app_query.fasta_1.1180 -LOSPCL=0 -LOÖPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=LOON-LIST=45 -DOCALIGN=200 -UNITS=bits -START=1 - START=1	Database: Published Applications NA:* 1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:* 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:* 3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:* 4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:* 4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*	5: /cgn2_6/ptodata/1/pubpna/USO7 NEW PUB.seq:* 6: /cgn2_6/ptodata/1/pubpna/USO7 NEW PUB.seq:* 7: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:* 8: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:* 9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:* 10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:* 11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:* 12: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:* 13: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:* 14: /cgn2_6/ptodata/1/pubpna/USIOR_NEW_Seq:* 15: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:* 16: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:* 16: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:* 17: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:* 18: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:* 18: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:*	19: /cgnz_e/ptcoara/l/pubpha/useu_ruscomb.seq:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Des.ilt (f.prv

```
1 651 100.0 702 15 US-0-287-460-27 Sequence 27, Appl. 651 100.0 1022 15 US-0-287-460-27 Sequence 27, Appl. 651 100.0 1022 15 US-0-287-460-27 Sequence 27, Appl. 651 100.0 1022 15 US-0-287-2724-3 Sequence 27, Appl. 651 100.0 2180 1 US-0-287-2724-3 Sequence 17, Appl. 651 100.0 2180 1 US-0-287-2724-3 Sequence 17, Appl. 651 100.0 2180 1 US-0-287-2724-3 Sequence 17, Appl. 10 US-0-287-100.0 2180 1 US-0-287-2724-3 Sequence 17, Appl. 10 US-0-287-100.0 2180 1 US-0-287-2724-3 Sequence 17, Appl. 11 US-0-287-100.0 2180 1 US-0-287-2724-3 Sequence 17, Appl. 11 US-0-287-100.0 2180 1 US-0-287-2724-3 Sequence 17, Appl. 11 US-0-287-2724-3 Sequence 17, Appl. 12 US-0-287-2724-3 Sequence 1822, Appl. 12 US-0-287-2724-3 Sequence 1822, Appl. 12 US-0-287-2724-3 Sequence 1822, Appl. 12 US-0-287-272-273-3 Sequence 1822, Appl. 12 US-0-287-1822 Sequence 1822, Appl.
```

```
11eThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyclnalaMetalaIlealaGlyclnIleargSerGlyclyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DIA

ORGANISM: Artificial Sequence

FRATURE:

OTHER INFORMATION: Description of Artificial Sequence:bi-fusion

OTHER INFORMATION: Erame 1

OTHER INFORMATION: Frame 1

NAME/KEX: CDS

IOCATION: (1)..(63)

OTHER INFORMATION: reading frame 1

NAME/KEX: CDS

IOCATION: (2)..(700)

OTHER INFORMATION: reading frame 2

NAME/KEX: CDS

IOCATION: (2)..(700)

OTHER INFORMATION: reading frame 2

NAME/KEX: CDS

IOCATION: (3)..(701)

OTHER INFORMATION: reading frame 3

IOCATION: (3)..(701)

OTHER INFORMATION: reading frame 3

US-09-287-849-27
                                                                                                                                                                                                                                                                                                                                                                                  702
1128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-684-215B-23 (1-128) x US-09-287-849-27 (1-702)
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SECTIANE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 ACAGGGAACGTGACATTGGCCGAG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27, Application US/10359460; Sequence 27, Application US/10359460; Publication No. US20030147911A1; GENERAL INFORMATION: APPLICANT: Skeiky, Yasir A.W.; APPLICANT: Alderson, Mark; APPLICANT: Alderson, Mark; APPLICANT: Campos-Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                                                  3.4e-69
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-10-359-460-27
                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

```
APPLICANT: Corixa Corporation; ITLE OF INVESTION: The Internation Proteins of Mycobacterium tuberculosis Antigens; ITLE OF INVESTION: and Internations of Internations and Internations of INVESTION: and Internations of INVESTION: and Internations of INVESTION: and Internations of Internations of Internations (10,003-00-005)

CURRENT APPLICATION NUMBER: US/09/207,449

PRIOR PAPLICATION NUMBER: US/09/207,449

PRIOR PAPLICATION NUMBER: US/09/207,197

PRIOR PALICATION NUMBER: US/09/207,197

PRIOR PALICATION NUMBER: US/09/207,197

PRIOR PALICATION NUMBER: US/09/207,197

PRIOR PILING DATE: 1997-04-07

PRIOR FILING DATE: 1997-04-07

PRIOR FILING DATE: 1998-12-30

PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 ileThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drecaledederededadederecedededadererededareredadedededes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlyBheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       710000
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-684-215B-23 (1-128) x US-10-359-460-27 (1-702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.4e-69
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             면
당 성
면
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     778 GICCAACGCGGGGGCGCGCGCGCGCGCAAGICTCGGCAATCTCCACCGGCGACGTG 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 ileThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  838 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        957
657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         718 Arcedeccracceccrrccrcecrreserrierereacaacaaceaaceaceacea 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                                                                                                                 898 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGCCCCCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Ra35 mature
10S-10-098-732A-3
                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-23 (1-128) x US-10-098-732A-3 (1-1002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               958 ACAGGGAACGTGACATTGGCCGAG 981
                                                121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                    385 ACAGGGAACGTGACATTGGCCGAG 408
                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           5.25e-69
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         챵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    요
                       g
                                               ò
                                                                В
```

Fusion Protein Constructs Comprising

APPLICANT: Skeaky, Yasir
APPLICANT: Skeaky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Brannon, Mark
APPLICANT: Gorderin Jeffrey
TITLE OF INVENTION: Heterologous Fusion Protes:
TITLE OF INVENTION: Leishmania Antigen
TITLE REFERENCE: 014058-012010US
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-01-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 1002

ORGANISM: Artificial Sequence

FEATURE:

Sequence 5, Application US/10098732A Publication No. US20030175294A1 GENERAL INFORMATION:

```
657
                                                                                                                                                                                                                                                                                                                      717
                                                                                                                                                                                                                                                                                                                                                                                       777
                                                                                                                                                                                                                                                                                                                                                                                                                                                          837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                      40
                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                               598 ACGCCCCCGTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                      21 GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                     718 ATCGGGCCTACCGCCTTCCTCGGCTTGGGGTGTTGTCGACAACAACGGCAACGGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      778 GTCCAACGCGTGCGCGCGCTCCCGCCCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 GlyHiBHiBProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                     1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaileProile
                                                                                                                                                                                                                                                                                                                                                          41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  898 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGGCGCACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                           61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/09712363
| Patent No. US20020164588A1 |
| RENEMAL INFORMATION: |
| APPLICANT: Eisenberg, David |
| APPLICANT: Rotstein, Sergio H. |
| APPLICANT: Marcotte, Edward M. |
| APPLICANT: Marcotte, Edward M. |
| TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
) OTHER INFORMATION: Description of Artificial Sequence:Ra35FLMutSAUS-10-098-732A-5
                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                     US-09-684-215B-23 (1-128) x US-10-098-732A-5 (1-1002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      958 ACAGGGAACGTGACATTGGCCGAG 981
                                                                  5.25e-69
651.00
100.00%
100.00%
                                                                                                  Percent Similarity:
Best Local Similarity:
                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-712-363-15
                                                                                                                                      Query Match
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                       8 B 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                         ઠ
```

```
81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 910 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGAGCGCGCTTAAC 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 GlyHisHisFroGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    670 ACGGCCGCGTCCGATAACTICCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGAIC 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1068
128
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215B-23 (1-128) x US-09-712-363-15 (1-1068)
FILE REFERENCE: 07419-032001

CURRENT APPLICATION NUMBER: US/09/712,363

CURRENT FILING DATE: 2000-11-13

PRIOR APPLICATION NUMBER: PCT/US00/02246

PRIOR APPLICATION NUMBER: 60/179,531

PRIOR FILING DATE: 2000-01-29

PRIOR FILING DATE: 1999-02-01

PRIOR FILING DATE: 1999-02-01

PRIOR FILING DATE: 1999-02-01

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-05-14

PRIOR FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 292

SEQ ID NO 15

LENGTHARE: FRALESEQ FOR WINGOWS Version 4.0

SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.67e-69
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 & B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              $ 8 $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
```

APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Corporation
TITLE OF INVENTOR Corporation
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILIG DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO(1)

TYPE: DNA ORGANISM: Artificial Sequence FEATURE:

LENGTH: 5281

```
81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           838 ATCACCGCGGTCGACGCCCCCCGATCAACTCCGCCCACCGCGATGGCGGACGCGCTTAAC 897
                                                                                                                                                                                                                                                       657
                                                                                                                                                                                                                                                                                                           777
                                                                                                                                                                                                                                                                                                                                                                                                                                   837
                                                                                                                                                                                                                                                                                                                                                                                                     61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                                                                                                                                                                                                                                                                                     40
                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                              41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                778 GICCAACGCGIGGICGCGAGCGCICCGGCGCGCAAGICICCGGCATCICCACCGGCGACGIG
                                                                                                                                                                                                                            1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyBheAlaIleProIle
                                                                                                                                                                                                                                                                                     21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-098-732A-17
Sequence 17, Application US/10098732A
PUBLICATION NO. US20030175294A1
GENERAL INFORMATION:
APPLICANT: Skelky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Cortxa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
OTHER INFORMATION: Description of Artificial Sequence: mutated COTHER INFORMATION: MTB32-MTB39F fusion protein (MTB32MutSA) US-10-369-983-1
                                                                                          2181
128
0
0
0
                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                               US-09-684-215B-23 (1-128) x US-10-369-983-1 (1-2181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       958 ACAGGGAACGIGACATTGGCCGAG 981
                                                                                     1.35e-68
651.00
100.00%
100.00%
                                                                                                           Percent Similarity: 1
Best Local Similarity: 1
Query Match: 1
DB:
                                                                            Alignment Scores:
                                                                                           Pred. No.:
                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                      8 8
                                                                                                                                                                                                                                                                                                                                                                                                 9 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             챵
```

970 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 1029

ద

ò

Sequence 1, Application US/10369983 Publication No. US20030235593A1 GENERAL INFORMATION: APPLICANT: Skeiky, Yasir

RESULT(6) US-10-369-983-1

```
US-US-Z8/-849-1

Sequence 1, Application US/09287849

Fatent No. US20020009459A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Reed, Steven G.

APPLICANT: Alderson Mark

APPLICANT: Campos Neto, Antonio

TITLE OF INVENTION: and Their Uses

TITLE OF INVENTION: and Their Uses

TITLE OF INVENTION: and Their Uses

TITLE OF INVENTION NUMBER: US 08/818,112

PRIOR PELICATION NUMBER: US 08/818,112

PRIOR APPLICATION NUMBER: US 08/818,112

PRIOR APPLICATION NUMBER: US 08/942,578

PRIOR APPLICATION NUMBER: US 08/925,197

PRIOR APPLICATION NUMBER: US 09/025,197

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGGGGGCGCGCGT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlydlnalaMetalailealaGlyGlnileArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                             41 IleGlyProThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                          Description of Artificial Sequence:MTB72FMutSA (Ra12-TbH9-Ra3SMutSA)
                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                             US-09-684-215B-23 (1-128) x US-10-098-732A-17 (1-2190)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 ACAGGGAACGTGACATTGGCCGAG 405
                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description
US-10-098-732A-17
                                                                                                                                                                                                                                 1.366-68
651.00
100.00%
100.00%
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 2190
                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-287-849-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 B
                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
```

```
243 GICCAACGCGIGGICGCGGAGCGCTCCGGCGGAAGICTCGGCATCTCCACCGGCGACGIG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAGACGGCAACGGCCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein Ra12-TbH9-Ra35 (designated Mtb32-Mtb39 OTHER INFORMATION: fusion)

NAME/KEY: modified_base
LOCATION: (30)

THER INFORMATION: n = g, a, c or t
NAME/KEY: modified_base
LOCATION: (33)

LOCATION: (42)...(2231)

LOCATION: (42)...(2231)

LOCATION: (42)...(2231)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2287
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-684-215B-23 (1-128) x US-09-287-849-1 (1-2287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10359460
Publication No. US203014/911A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
                                                                                                                                                                                                                                                                                                                                                                                         ц
                                                                                                                                                                                                                                                                                                                                                                                         ö
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2287
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                           U
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.43e-68
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                       ) LOCATION: (2270)
; OTHER INFORMATION: n = g, a,
US-09-287-849-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-359-460-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

09/223,040

3 06:36:18 Z004

mon may

```
303 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCCTTAAC 362
                                                                                                                                                                                                                                                 RESULT 10
US-10-08-732A-15
i Sequence 15, Application US/10098732A
j Publication No. US20030175294A1
j GENERAL INFORMATION:
i GENERAL INFORMATION:
j APPLICANT: Skeiky, Yasir
j APPLICANT: Guderian, Jeffrey
j APPLICANT: Guderian, Jeffrey
j APPLICANT: Guderian, Jeffrey
j TILE OF INVENTION: Leishmania Antigen
j TILE OF INVENTION Hereologous Pusion Protein Constructs Comprising a
j TILE OF INVENTION Leishmania Antigen
j FILE REFERENCE: 014058-012010US
j CURRENT APPLICATION NUMBER: US/10/098,732A
j PRIOR FILING DATE: 2003-04-29
j PRIOR FILING DATE: 2001-03-13
j NUMBER OF SEQ ID NOS: 80
j SOFTWARE: PatentIn Ver. 2.1
j SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlyGerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                   GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein MTB72F (Ra12-TbH9-Ra35 or MTB32-WTB39 OTHER INFORMATION: fusion)
FEATURE:
NAME/KEY: CDS
COCATION: (42)...(2231)
COCATION: (42)...(2231)
FRATURE:
NAME/KEY: modified base
LOCATION: (1)...(2287)
CTHER INFORMATION: n = g, a, c or t
US-10-098-732A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2287
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-23 (1-128) x US-10-098-732A-15 (1-2287)
                                                                                                                                                            121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                       423 ACAGGGAACGTGACATTGGCCGAG 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score: 1.43e-68
Score: 651.00
Percent Similarity: 100.00%
Dest Local Similarity: 100.00%
Ouery Match: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                          101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                               셤
                                                                                                                                                     ठ
  APPLICANT: Campos-Neto, Antonio
APPLICANT: Canpos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: and Their Uses
FILLE REPRENCE: 01408-0020208
CURRENT PLING DATE: 2003-02-05
CURRENT APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-00-01
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2287
1287
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-684-215B-23 (1-128) x US-10-359-460-1 (1-2287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: modified_base
LOCATION: (33)
OTHER INFORMATION: n = g, a, c or
FEATURE:
LOCATION: (42)...(2231)
FEATURE:
LOCATION: (42)...(2231)
FEATURE:
LOCATION: (2270)
OTHER INFORMATION: n = g, a, c or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.43e-68
651.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-359-460-1
```

242

9

302

80

122

QQ δ g ð g ઠે

-

```
81 IlethralavalaspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                25 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGGAGAGGATTCGCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 IleGlyProThrAlaPheLeuGlyVeuUGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 GTCCAACGCGTGGGGGGGGGCGCTCCGGCAAGTCTCGGCATCTCCACGGCGACGTG
1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                           61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA (CROANISM: Artificial Sequence) (CROANISM: Artificial Sequence) (CROANISM: Artificial Sequence: FEATURE: ) OTHER INFORMATION: MIBSIF (WIB72F-DPV) (CREER INFORMATION: MIBSIF (WIB72F-DPV)
                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-10-369-983-8
US-10-369-983-8
Sequence 9, Application US/10369983
Publication No. US20030235593A1
SEMENAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Greek, Steven
APPLICANT: Corios Corporation
FILE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPREMENCE: 0.4608-009081US
FILE REPREMENCE: 0.4068-009081US
CURRENT FILING DATE: 2003-02-18
FRIOR PRILING DATE: 2003-02-15
NUMBER: OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
ILBURITH: 2451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2451
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-215B-23 (1-128) x US-10-369-983-8 (1-2451)
                                                                                                                                                                                                                                                                                                                423 ACAGGGAACGTGACATTGGCCGAG 446
                                                                                                                                                                                                                                                                                          ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1,56e-68
651.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                        183
                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     · 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                 6 6 6 6 6 6
                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                             Welloating the Marketter of the Markette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                            303 ATCACCGGGTCGACGGCGCTCCGATCAACTCGGCCACGCGGATGGCGGACGCGCTTAAC 362
                                                                             GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                          21 GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2287
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-684-215B-23 (1-128) x US-10-359-459-1 (1-2287)
                                                                                                                                                       1.43e-68
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41
        81
                                                                               101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                              g
                                      g
                                                                               à
                                                                                                                                                       Š
                                                                                                                                                                                            g
        ઠે
```

204

9

20 84 264

265 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 324

```
81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 Arcaccececreacecercearcearcaacresecreesearesecearesecearesecrivae 324
                         61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGheAlalleProlle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGGCGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 GICCAACGCGTGGICGGGAGCGCTCCGGCGGCAACTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                           Sequence 7, Application US/10369983
; Bublication No. US2003023553A1
; Bublication No. US2003023553A1
; Bublication No. US2003023553A1
; APPLICANT: SKeiky, Yasir
; APPLICANT: Guderian, Jeff
; APPLICANT: Guderian, Jeff
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; FILE REPREMENCE: 014658-00908A1US
; FILE REPREMENCE: 014658-00908A1US
; CURRENT APPLICATION NUMBER: US/10/369,983
; CURRENT FILING DATE: 2003-02-18
; PRIOR FILING DATE: 2002-02-15
; NUMBER: OF SEQ ID NOS: 22
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 7
: INROTH: 2487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence CRANISM: Artificial Sequence: PEATURE: PEATURE: OTHER INFORMATION: Description of Artificial Sequence:fusion protein US-10-369-983-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2487
0 0
0 0
0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-684-215B-23 (1-128) x US-10-369-983-7 (1-2487)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrGlyAsnValThrLeuAlaGlu 128
                                                                 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                              385 ACAGGGAACGTGACATTGGCCGAG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.59e-68
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
101
                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                           g
                                                                 ሯ
                                                                                             g
à
```

```
101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 IleThralaValaspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 GICCAACGCGGGGGGGGGGGCCCCGGCGGCAAGICICGGCATCTCCACCGGCGACGTG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACGCGGATGGCGGGACGCGTTAAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 Acescoecorcosaracriccascrereceassassassassasaricsccarreceare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
RESULT 14

US-10-369-983-6

US-10-369-983-6

US-Quence 6, Application US/10369983

Publication No. US20030235593A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Guderian, Jeff

APPLICANT: Graven

TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

CURRENT APPLICATION NUMBER: US 40/359,983

CURRENT APPLICATION NUMBER: US 60/357,351

PRIOR FILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 2637
                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: MTB89F (MTB72F-Erd14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2637
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215B-23 (1-128) x US-10-369-983-6 (1-2637)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 64, Application US/10098732A
Publication No. US20030175294A1
GENERAL INPORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.7e-68
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-369-983-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 පු පු
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         중 음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   요 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ठे
```

144

84

9

204

```
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                       .. ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arcaccecerceacececrecearcacreeccacecearececearececercecerraac 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               descarcarceces reacercarcic estas es
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Description of Artificial Sequence:WTB72F-MAPS; OTHER INFORMATION: (r95f) fusion construct, TB MTB72F (Kal2-TbH9-Ra35); OTHER INFORMATION: linked to Leishmania thiol-specific antioxidant; OTHER INFORMATION: (TSA or MAPS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising of TITLE OF INVENTION: Leishmania Antigen
FILE REPERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR APPLICATION NUMBER: US 60/275,837
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 64
LENTIN: 2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10369983
Publication No. US2003023559341
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2808
128
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-23 (1-128) x US-10-098-732A-64 (1-2808)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAGGGAACGTGACATTGGCCGAG 408
                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: (1951) fus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.84e-68
651.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 16
US-10-369-983-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
```

```
81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 Arcadaceracedecerecerenegerererenegacaacaacaaceaceaceacea 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 erccaacecereerceeaacecrcceeceaaarcrceecarcrceecarcrcacaceeceacere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 Aceeccecerceanaactrccaecterccaeegreeecaeegarrceccarrccearc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:MTB-102F fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Skeiky, Yaair
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Grats
Guderian, Jeff
APPLICANT: Grats
APPLICANT: Grats
Corporation
TILE REPERRICE: 014058-00981US
FILE REFERRICE: 014058-00981US
CURRENT FILING DATE: 2002-02-18
PRIOR PILING DATE: 2002-02-18
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                                CTHER INFORMATION: Description of Artificial Sequence:fusion protein; OTHER INFORMATION: R95F (MTB72F-MAPS)
US-10-369-983-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIl
                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-23 (1-128) x US-10-369-983-5 (1-2808)
                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385 Acadddaacdrdacarrddccdad 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10369983
Publication No. US20030235593A1
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 2808
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                              1.84e-68
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-369-983-3
```

```
GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                         144
                                                                                                                                                                                                                                                                                                      205 GICCAACGCGIGGICGGGAGCGCICCGGCGGAAGICICGGCAICTCCACCGGCGACGIG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleThralaValaspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 Arcaccecesrceacescerrecearcaacreseceacesceacesareseces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                             84
                                                                                                                                                                              40
                                                                                                                                                                                                                                                                          90
                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25. Aceeccecetrocataactrocaecterceaegargescaaggarroscatocato
                                                                                                                                                                           21 GlyGlnAlaMetAlaileAlaGlyGlnileArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                       85 dedchededangecearcecedencearcearcearcegecedededececececercar
                                                                                                                                  25 Aceaccacarceanaachicaachachacaacaacaacaancacanc
                                                                                                                                                                                                                                                                            41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                         61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             us-lu-say-bs-lu-no VS2030235593A1
Sequence 10, Application US/10369983
Publication No. US2030225593A1
Sequence 10, Application WS2030235593A1
Sequence 10, Vasir
Sedivarion:
APPLICANT: Skeiky, Yasir
APPLICANT: Corixa Corporation
TITLE OF INVENTION Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERBURE: 014058-009081US
CURRENT APPLICATION NUMBER: US 60/357,351
FRIOR APPLICATION NUMBER: US 60/357,351
FRIOR APPLICATION NUMBER: US 60/357,351
FRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 3104
TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
FRATURE:
CHER INFORMATION: Description of Artificial Sequence:
FEATURE:
CHER INFORMATION: MIBBIOLEMER (MIBBIOLETM, MIB72F-HTCC#1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description of Artificial Sequence:fusion protein MTB102tm2F (MTB102FTM, MTB72F-hTCC#1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3104
0 0 0
0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-23 (1-128) x US-10-369-983-10 (1-3104)
                                   US-09-684-215B-23 (1-128) x US-10-369-983-11 (1-3060)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 ACAGGGAACGTGACATTGGCCGAG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.08e-68
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 19
US-10-369-983-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-369-983-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               유 상
                                                                                 ò
                                                                                                                          셤
                                                                                                                                                                                   à
                                                                                                                                                                                                                         요
                                                                                                                                                                                                                                                                     \overset{\diamond}{\circ}
                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                            ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 IleThralaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       835 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAAC 894
                                                                                                                                                                                                                                                                                                                                                       654
                                                                                                                                                                                                                                                                                                                                                                                                                                              715 Arcedectraccecerrecerrederriedererreteachachacecheececeche 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              834
                                                                                                                                                                                                                                                                                                                                                                                                     21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                       ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                           ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/10369983

Sequence 11, Application US/10369983

FUDICATION NO. US20030235593A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US 10/10/369,983
CURRENT PILING DATE: 2002-01-18
FRIOR APPLICATION NUMBER: US 60/357,351
FRIOR PILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence:fusion protein; OTHER INFORMATION: MTB103F (MTB72F-85b)
US-10-369-983-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3060
128
0
0
                                                                                         3030
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                             US-09-684-215B-23 (1-128) x US-10-369-983-3 (1-3030)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.04e-68
651.00
100.00%
100.00%
                                                                                    2.02e-68
651.00
100.00%
100.00%
; OTHER INFORMATION: protein US-10-369-983-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                        655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
```

ò 셤 ઠે d à q à 셤

ò g ò g ઠે 셤

Db 205 GTCCAACGCGTGGTCGGGGGCAAGTCTCGGCATCTCCACCGGCGACGTG 264	RESULT 21 US-10-193-002-4 ; Sequence 4, Application US/10193002 ; Publication No. US20030135026A1 ; GENERAL INFORMATION: ; APPLICANT: Reed, Steven G. ; APPLICANT: Reed, Steven G. ; Dillon, Davin C.	; Campos-Neco, Antonia ; Houghton, Raymond ; Vedvick, Thomas S. ; Twardzik, Daniel R. ; Lodes, Michael R. ; Hendrickson, Ronald C. ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF ; TITLE OF INVENTION: TUBERCILOSIS	JENCES: SADDRES: SEEI 3300 Cc	: py disk compatible PC-DOS/MS-DOS	SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/193,002 FILING DATE: 10-701-2002 CLASSIFICATION: <unknown> PRIOR APPLICATION: <unknown> PRIOR APPLICATION: <unknown> APPLICATION: WINNERD: ING/00/072,506</unknown></unknown></unknown>	LON NOMBER: 05/05/07/2/59 TINFORMATION: i, David J. TION NUMBER: 21,392 TION INFORMATION: TION INFORMATION: E: (206) 622-4900	INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH 447 base pairs TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid	SEQUE -002-	Alignment Scores: 7.87e-69 Length: 447 Pred. No.: 646.00 Matches: 127 Score: 646.00 Conservative: 0 Bercent Similarity: 99.22\$ Mismatches: 1 Query Match: 159.23\$ Indels: 0 DB: 15
	Db 265 ArcAccecedreacedcercearcaarcaacerceacearceacearcaacearcaacerraac 324 Oy 101 GlyHisHisProclyAspValileSerValThrTrpGlnThrLvsSerGlyGlyThrArg 120 Db 325 GeoCATCATCCCCGCTGACGTCATCTCCGGTGAACCTGGCAACCGAGTCGGCGCGCGC	RESULT 20 US-10-369-983-9 Sequence 9, Application US/10369983 Publication No. US20030235593A1 GENERAL INFORMATION: APPLICANT: SHeiky, Yasir APPLICANT: SHeiky, Yasir) AFFLICANT: Read, Steven) APPLICANT: Read, Steven) APPLICANT: Corixa Corporation ; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis ; FILE REFERENCE: 014058-009081US ; CURRENT APPLICATION NUMBER: US/10/369,983 ; CURRENT APPLICATION 104TR: 20013-02-18	PRIOR APPLICATION NUMBER: US 60/357,351 PRIOR FILING DATE: 2002-02-15 NUMBER OF SEQ ID NOS: 22 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 9	TYPE: DNA CRGANISM: Artificial Sequence FEATURE: CHER INFORMATION: Description of Artificial Sequence:fusion protein CHER INFORMATION: MTB114F (MTB72F-mTCC#2) US-10-369-983-9	Alignment Scores: 2.39e-68 Length: 3474 Score: 651.00 Matches: 128 Percent Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Mismatches: 0 DB: 16 Gaps: 0	US-09-684-215B-23 (1-128) x US-10-369-983-9 (1-3474) QY	Oy 21 GlyGlnalaMetalarlealaglyGlnIleArgSerGlyGlyGlySerProThrValHis 40	41 145 61

```
Sequence 9, Application US/10098732A;
Sequence 9, Application US/20030175294A1

Sequence 9, Application No. US20030175294A1

Publication No. US20030175294A1

APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeffrey
APPLICANT: Gratian Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29

PRICR PLING DATE: 2001-03-13
PRICR PLING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80

CURRENT ATTÉ: DNA

ORGANISM: Artificial Sequence
FEATURE:
CHER INFORMATION: C-terminus)

OTHER INFORMATION: C-terminus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            driczkacecoredakacecriceededakaricricecarcricedakiere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 ileThrAlaValAspGlyAlaProileAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGGTCACCCACGTTCAT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACAACGGCAACGGCACGA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlyGsProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 Archicecearcearcearcearcaarcaachceaceaceacearcecearcecearce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 GGGCATCATCCGGTGATCTCGGTGAACTGGCAAACCAAGTCGGGCGGCACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle
                                                                                                                                                                                                                                                                                                                                                               44
10
10
10
00
                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-23 (1-128) x US-10-084-843-4 (1-447)
                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 ACAGGGAACGTGACATTGGCCGAG 394
                                                                                                                                                                                                                                      ö
                                                                                                                                                                   TOPOLOGY: single TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID US-10-084-843-4
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                      7.876-69
646.00
99.22%
99.22%
99.22%
                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 23
US-10-098-732A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 dedecarcarcacederarentarente de arcade da arcade da arcade de arcade de arcade de arcade de arcade arca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyHisHisProGlyAspValileServalThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                  Greenardedrogandederectedededandrectededarctededadadada 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 IleThralaValaspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arcaccecedenceacecricearcaacreeceacecedencededeacecerraac 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                                                                                                                                                                                                                                             40
                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                             20
                                                                                                                                                                      70
                                                                                                             ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                             21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky, Yasir A.W.

Dillon, Davin C.
Campos.Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 500 Columbia Center, 701 Fifth Avenue
CITY: Seattle
CITY: Seattle
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION NUMBER: US/10/084,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MXY-1998
ATTORNEY, AGENT INFORMATION:
NAME: MAKA, DAVIG J.
REGISTRATION NUMBER: 31,392
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                 US-09-684-215B-23 (1-128) x US-10-193-002-4 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 22
US-10-084-843-4
; Sequence 4, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

g 6

ઠે

셤

ò 셤

OD 8

8

ð

310

9

```
PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                       190
                                                                                                                                                                                                                            71 GGGCAGGCGATGGCGATCGCGGGCCAGATCGATCGGGTGGGGGGTCACCCATCAT 130
                                                                                                                                                                                                                                                                                                              81 IleThralaValAspGlyAlaProlleAsnSerAlaThralaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                 251 ATCACCGGGGTCGACGGCGCTCCGATCAACTCGGCCACGCGGATGGCGGGATGAC 310
                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                        40
                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                            41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                          21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/10193002

Publication No. US20030135026A1

BENERAL INFORMATION:

APPLICANT: Reed, Steven G.

Beiky, Yasir A.W.

Dillon, Davin C.

Campos-Neto, Antonia

Houghton, Raymond

Vedvick, Thomas S.

Twardzik, Daniel R.

Lodges, Michael J.

Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF

TUBERCULOSIS

TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 350

CORRESPONDENCE ADDRESS:
ADDRESSES: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <UNKNOWN>
                                        444
0 0 1 2 7 0 0 0 0 0 0
                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                               US-09-684-215B-23 (1-128) x US-10-098-732A-9 (1-447)
                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ThrGlyAsnValThrLeuAlaGlu 128
                                    7.87e-69
646.00
99.22*
99.22*
                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-10-098-732A-9
                         Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 24
US-10-193-002-17
                                                                                                                                                                            g
                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                        ò
                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
998 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 25
US-10-084-843-17
Sequence 17, Application US/10084843
Sequence 17, Application Wo US20030143243A1
Sevence 18, Steven G.
Selvence 18, Yasia A.W.
Dillon, Davin C.
Campos Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Thardalk, Daniel R.
Lodes, Michel J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GlyGlnAlaMetAlaIleAlaGlyGlnGleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1058 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGGGGGCACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                         1872
127
0
0
0
APPLICATION UNMER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 21.392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELERAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: USPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-193-002-17
                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-684-215B-23 (1-128) x US-10-193-002-17 (1-1872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1118 ACAGGGAACGTGACATTGGCCGAG 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ThrGlyAsnValThrLeuAlaglu 128
                                                                                                                                                                                                                                                                                                                                                           Pred. No.: 4.5e-68
Score: 646.00
Percent Similarity: 99.22*
Query Match: 99.23*
DB: 15
                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
```

```
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSES SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STRIE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER: PROPA disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/084,843
FILING DATE: 55-Feb-2002
CLASSITICATION NUMBER: US/09/072,967
FILING DATE: 55-Feb-2002
CLASSITICATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/COCKET NUMBER: 210121.411C9
FILEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: CRAMATION:
TELEPHONE: CRAMATION:
TELEPHONE: CRAMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: CRAMATION:
TELEPHONE: CRAMATICS:
SEQUENCE CHARACTERISTICS:
LENGTH 1872 base pairs
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
```

| Sequence 1, Application US/10099732A | Sequence 1, Application US/10099732A | Publication No. US20030172294Al | Publication No. US20030172294Al | Publication No. US20030175294Al | GENERAL INVORMATION | APPLICANT: Skeiky, Yasir | APPLICANT: Skeiky, Yasir | APPLICANT: Guderian, Jeffrey | APPLICANT: Guderian, Jeffrey | APPLICANT: Grown Corporation | TITLE OF INVENTION: Leishmania Antigen | TITLE OF INVENTION: Leishmania Antigen | TITLE OF INVENTION: Leishmania Antigen | FILE REFERENCE: 104058-012010US | CURRENT FILING DATE: 2003-04-29 | PRIOR APPLICATION NUMBER: US 60/275,837 | PRIOR APPLICATION NUMBER: US 60/275,837 | PRIOR PLING DATE: 2001-03-13 | NUMBER OF SEQ ID NOS: 80 | SOUTHARE: Patentin Ver. 2.1 | SEQ ID NO 1 | LENGTH: 1872 | LENGTH: 1872

	1872	127	0	т	0	0	
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:	
	4.5e-68	646.00	99.22%	99.22%	99.23%	15	
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	

Length:
Matches:
Conservative:
Mismatches:
Indels:

Pred. No.: 4.5e-68 Score: 646.00 Percent Similarity: 99.22* Best Local Similarity: 99.23* Query Match: 99.23*

Alignment Scores:

TYPE: DNA

ORGANISM: Mycobacterium tuberculosis

FEATURE:
OTHER INFORMATION: MTB32A (Ra35FL)
FEATURE:
NAME/KEY: modified base
LOCATION: (1). (1872)
OTHER INFORMATION: n = g, a, c or t
US-10-098-732A-1

US-09-684-215B-23 (1-128) x US-10-084-843-17 (1-1872)

à	1 ThrAlaAle	ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProlle 20
qa	758 ACGGCCGC	ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC 817
ò	21 GlyGlnAle	GlyGlnAlaMetAla1leAlaGlyGln1leArgSerGlyGlyGlySerProThrValHis 40
Db	818 GGGCAGGCC	GGGCAGGCGATGGCGATCGCGGGCCAAATCCGATCGGGTGGGGGGGTCACCCACC
ò	41 IleGlyPro	lleGlyProThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
Dp	878 ATCGGGCC	ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 937
λ̈	61 ValGlnArg	ValGinArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
qa	938 GTCCAACG	GTCCAACGCGTGGTCGGAAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGGCACGTG 997
λò	81 IleThrAl	lleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
qq	998 ATCACCGC	ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 1057
ò	101 GlyHiBHi	GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
q	1058 GGGCATCA	GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGCACGCGT 1117
δλ	121 ThrGlyAs	ThrdlyAsnValThrLeuAlaGlu 128
QQ	1118 ACAGGGAA	ACAGGGAACGTGACATTGGCCGAG 1141

```
1058 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGGCACGCGT 1117
                                                                                                                                                                                                                                                                                                                       101 GlyHisHisBroGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                 41 IleGlyProfhrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGerProThrValHis 40
                                                                                                  1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProI
1872
1127
0
0
0
                                                                           US-09-684-215B-23 (1-128) x US-10-098-732A-1 (1-1872)
                                                                                                                                                                                                                                                                                                                                                                                         1118 ACAGGGAACGTGACATTGGCCGAG 1141
                                                                                                                                                                                                                                                                                                                                                                    121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 27
US-09-759-143-822
'Sequence 822, Application US/09759143
'Patent No. US20020022248A1
                                              Query Match:
DB:
                                                                                                   ઠે
                                                                                                                   g
                                                                                                                                         à
                                                                                                                                                                g
                                                                                                                                                                                  ð
                                                                                                                                                                                                           g
                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                          ठ
                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                          ઠ્ઠ
                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                     ሯ
```

18-08-09-40-40-80-80-81

\$007 ST:95:90 5

Mon may

```
GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 ACGGCGCGTCCCATACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC 81
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Handerson, Robert A.
APPLICANT: Handerson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Darrick
APPLICANT: Gart K.
APPLICANT: Gart K.
APPLICANT: Gart C.
APPLICANT: Wang, Aljun
APPLICANT

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      675
1122
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-23 (1-128) x US-09-759-143-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.97e-64
608.00
96.09$
95.31$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-09-759-143-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:

Pred. No.:
Score:
Percent Similarity:
Guery Match:
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAG-----CTTCCCACCGTTCAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 IleThralaValaspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE THERAPY AND
GRUNEAL INFORMATION.

GRUNEAL INFORMATION.

APPLICANT: Mitcham, Davin C.

APPLICANT: Mitcham, Davin C.

APPLICANT: Mitcham, Davin C.

APPLICANT: Handcker, Susan L.

APPLICANT: Handcren, Fobert A.

APPLICANT: Henderson, Robert A.

APPLICANT: Rederson, Robert A.

APPLICANT: Rederson, Robert A.

APPLICANT: Rederson, Robert B.

APPLICANT: Rederson, Robert B.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Henderson, Raymond L.

APPLICANT: Handly Abelicant Beller, William

APPLICANT: Howell, John A.

APPLICANT: Howell, Particia D.

APPLICANT: Howel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                675
122
1
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-23 (1-128) x US-09-780-669-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGGGAACGTGACATTGGCCGAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.97e-64
608.00
96.09%
95.31%
93.39%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CRGANISM: Homo sapiens
US-09-780-669-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                장염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               원
```

81 40 9

29

RESULT

ò

RESULT 28 US-09-780-669-822 Sequence 822, Application US/09780669 ; Patent No. US20020051977A1

```
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hural, John
APPLICANT: Hural, John
APPLICANT: Moneill, Patricia D.
APPLICANT: Wingle de Bassols, Carlota
APPLICANT: Vingle de Bassols, Carlota
APPLICANT: Poy, Teresa
APPLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-09-895-793-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 ACGGCCCCGGTCCCGATAACTTCCCAGCTGTCCCAGGGTGGGCAGGAATTCGCCATTCCCAATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                       THE THERAPY AND
         US-09-822-827.822

Sequence 822, Application US/09822827

Fatent No. US20020081680A1

GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

CURRENT APPLICATION UNMER: 108/09/822,827

CURRENT APPLICATION UNMER: 2001-03-28

NUMBER OF SEQ ID NOS: 982

LENGTH: 675

TENGTH: 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-23 (1-128) x US-09-822-827-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 822, Application US/09895793;
Publication No. US20020192763A1;
GENERAL INFORMATION:
APPLICANT: Yu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Stols, Michael D.
APPLICANT: Stols, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 ACAGGGAACGTGACATTGGCCGAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.97e-64
608.00
96.09%
95.31%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
Percent Similarity:
Best Local Similarity: 9
Ouery Match:
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 30
US-09-895-793-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 & 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             & 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \delta
```

```
129
                                                                                                                 101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                           81
                                                                                        40
                                                                                        310 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGGGGCACGCGT
     675
1122
11
14
     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                    US-09-684-215B-23 (1-128) x US-09-895-793-822 (1-675)
                                                                                                                                                                                                                                                        Search completed: April 30, 2004, 05:10:29 Job time : 474.379 secs
    4.97e-64
608.00
96.09%
95.31%
93.39%
Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                  8 8 8
                                                                                                                                                                                                          셤
                                                               ò
                                                                          셤
                                                                                      ઠે
                                                                                                   염 장
                                                                                                                             셤
                                                                                                                                         8 &
```

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

(without alignments) 1524.660 Million cell updates/sec April 29, 2004, 22:25:27; Search time 2507.02 Seconds OM protein - nucleic search, using frame_plus_p2n model Run on:

651 1 TAASDNFQLSQGGGFAIPI......SVTWQTKSGGTRTGNVTLAE 128 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext US-09-684-215B-23 **BLOSUM62** Title: Perfect score: Scoring table: Sequence:

55026578 27513289 segs, 14931090276 residues Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

em_esthum: *
em_estin: *
em_estin: *
em_estin: *
em_estpl: *
em_estpl: *
em_bc: *
em_bc: *
gb_est: *
gb_est: *
gb_est: *
gb_est: *
gb_est: * estom:* em estba:* Ea

em_gss_inv:* em_gss_pln:* em gas hum: *

em gss vrt:*
em gss fun:*
em gss mam:*
em gss mus:* em_gss_rod:.*
em_gss_rod:.*
em_gss_rod:.*
gb_gss_vrl:.*

gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	U82114 or	73	BZ549048 pacs1-60_	7918	2560	2890	3442	38	23	3	2	7	8	S	5	= :	10	40.0	7 5	4 6	100	BI378928 BFLG1 000	9	끔	6	BJ285991 BJ285991	457 OGQAF7	71201	•	74407	10000	1 0	BZ576076 msh2 4761	97044	722	78796	71516	4057	3664B fu8(79512 faa	64397 ZF0(95047 £k28	512107 CAbi
	DI DI	211	77079	904	57918	92560	2890		BQ514888	CD080132	BZ561390	BZ549047	AQ989479	AZ933900	AJ558965	CA480614	AI597611	BI350520	CA473840	CA148171	0112114	AWZ65510	BI378928	CA975497	CF787130	3	ŝ	CC345457	CA471201	CF265501	CA4 / 446 V	, . , .	16		27	7	9,	7.15	740	BM036648	795	3643	5950	513
	נס	289 2	38 2	59 2	26 1	90 1	1 10	33 28	58 13	32 14	33 28	47 28	26 28	19 28	55	59 14	23 9	99 12	70 14	44 44 44 44	7 .	910	677 12	09 14	00 14	47 l	28 1	00	1 20	13	70	200	20	4 6	766 1	06	94	99	52 1	13 1	55 1	70 1	13 1	11
de	ery tch L	2.4	4.6	œ.	œ,	œ,	۲.	7.	7.	16.6	6.4	'n	'n.	15.7	'n.	'n	ь О	٠ س	'n.				14.7	4	4.	4.	4.	4.	4.	4.		4, 4	; <		4	4	4	4	4.	4.	4	4	4	. 4
	ŭ		26.	N	20.		15.	~	-4	O	96.		C	102	2		σ	97.5	۲,	700	7	9 4	ָ ה ה	6	4.	4.	94.5	m.	<u>.</u>	m, (ກ ເ	vi c	i.	100	. 5	92	92	92	H	ä	91.5	ä	H	, -
	Sul			n U		S	9		&	6	-	c 11	12	13	14	c 12	16	c 17	-	т С	9 6	7.7	7 6	ı (N	c 55	N	N	N	CN (0 m 0	י ניי	יו ני	ን ሮ	יי ר	36	1 M	38	m	4	4	c 42	4	4	

ALIGNMENTS

U82114 ordered cosmid library Mycobacterium leprae genomic clone cosmid L-373; contig 64, genomic survey sequence. U82114.1 GI:3647212 **UB2114** RESULT 1 U82114 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION

Mycobacterium leprae Mycobacterium leprae Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corymebacterinese, Mycobacteriaceae, Mycobacterium.

REFERENCE

```
BH770798 linear GSS 01-MAY-2002 LLMGtag541 MG1363 Random Sequence Tag Library Lactococcus lactis ubsp. cremoris genomic, genomic survey sequence.
BH770798 GI:20373755
Silbaq,F.S., Cho,S.N., Cole,S.T. and Brennan,P.J.
Characterization of a 34-kilodalton protein of Mycobacterium leprae
that is isologous to the immunodominant 34-kilodalton antigen of
Mycobacterium paratuberculogis
Infect. Immun. 66 (11), 5576-5579 (1998)
                                                                                                                         Colorado State University
Fort Collins, CO 80523, USA
Eiglmeier, K., Honore, N., Woods, S.A., Caudron, B. and Cole, S.T. Use
of an ordered cosmid library to deduce the genomic organization of
Mycobacterium leprae. Mol. Microbiol. 7 (2), 197-206 (1993)
Class: unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 ValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHis 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsn---GlyAlaArgValGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Val ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactococcus lactis subsp. cremoris
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1438)
Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments (2002) In press
Contact: Sorokin A
Genetique Microbienne
                                                                                                                                                                                                                                                                                                                                                                                      1..289
/organism="Mycobacterium leprae"
/mol_type="genomic DNA"
/db xref="taxon:1769"
/clone="cosmid L-373; contig 64"
/clone_lib="ordered cosmid library"
                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-684-215B-23 (1-128) x U82114 (1-289)
                                                                                                                                                                                                                      ass: unknown.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValThrieuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grcacacrceccaag 261
                                                                                                                                                                                                                                                                                                                                                                                      6.63e-05
145.50
58.828
41.188
                                                                                                          Contact: Silbag FS
Microbiology
                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                              9784577
                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH770798/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                              JOURNAL
MEDLINE
PUBMED
    AUTHORS
TITLE
                                                                                                                                                                                                                                    FEATURES
                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
pacs1-60 1644.s2 pacs1-60 Pecudomonas aeruginosa genomic clone pacs1-60 1644, genomic survey sequence. BZ549048. BZ549048.1 GI:27152629 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 AspalaLeuAsnGlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSer 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 959)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTTTAGGTTTTGCTATCCCATCTAATGATGTGGTAAAACATCATTAATAACTTGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 AGTGCTCTTTACTCACAGATATTAATGATACTGTGAAAGTCACCTACTACTAC---CGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 GACCTATCTCAATTATCAACAAATGATAGTTCTCAACTGAAATTACCTAGCAGCGTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 ---GlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 ThrolyAspValileThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAla
      cedex, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyGlnGlyPheAlaileProileGlyGlnAlaMetAlaileAlaGlyGlnIleArgSer
                                                                                                                                                                                                                 /sub species="cremoris"
/db_xref="taxon:1359"
/clone lib="Mq1363 Random Sequence Tag Library"
/clone="toctor: pSGWU2; Site 1: Smal; Library of
/note="Vector: pSGWU2; Site 1: Smal; Library of
chromosomal fragments of L. Tactis strain MG1363 was
prepared by partial AluI digestion or by sonication."
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, F. Tel: 33 134 65 25 16
Fax: 33 134 65 25 21
Email: sorokine@jouv.inra.fr
best homologue in strain IL1403 is htrA (95%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 1408.
Location/Qualifiers
1. 1438
1. 1438
And Lype="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/strain="MG1363"
                                                                                                                                                                                                                                                                                                                                                                   144
240
240
8
8
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asp------AsnAsnGlyAsn-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 GlyGlyThrArgThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 GGTAAATCAGCCACAGCAAATGTCAAACTCTCTAAA 105
                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-23 (1-128) x BH770798 (1-1438)
                                                                                                                                                                                                                                                                                                                                                                     0.0521
126.50
45.45%
30.30%
                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 GATGGT
                                                                                                                                                                                                                                                                                                                                                         Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
BZ549048/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                     No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                         Alignment
                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>Q</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ें
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \dot{\delta}
```

us-09-684-215b-23.rst

```
/clone lib="OSJNBf"
hote="Vector: pBluesript II KS +; Site_1: EcoRI; Site_2:
Xhof; Uninfected Control"
                                                           Mazur, E.,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (Bases 1 to 726)
38 Jantaeuriyarat, 726)
39 Jantaeuriyarat, 726, Lu,G., Gowda,M., Harfield,J., Zhou,B., Mazur,E., Large-scale identification of ESTe involved in the interaction between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
Rols: 520 626 3967
Far: 520 626 3967
Far: 520 626 3967
Far: 520 626 3967
Far: For Figure 1 Popularion Rodu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThralaMetalaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerValThrTrp 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 Gricciógogocagiociócadecadasciógiciigirectaceagragogoringer 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ileSerThrGlyAspValileThrAlaValAspGlyAlaProileAsnSerAla 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GlyGlnIleArgSerGlyGlyGlySerProThrValHisIleGlyPro 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 ThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 genaccárrientenregigarencarrencereceregacegraaccharcaaagecaaa
                                                                                                                                                                                                                                                                                                                                                                                 1. 726.

/organism="Oryza sativa (japonica cultivar-group)"

/orlivar="Wipponbare"

/cultivar="Wipponbare"

/db_xref="taxon:39947"

/clone="OSNNEf02F19"

/tissue_type="Leaf"

/dev stagge="3 week"

/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 SerGlnGlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAla-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GinThriysSerGlyGlyThrArgThrGlyAsnValThrieu 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 CAAAGA-----GGCGCTGAATCTCTGGAGGTAACCTTG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ValValGlySerAlaProAlaAlaSerLeuGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                              FORWARD: gra aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 02 row: F column: 19
Seg primer: gga aac agc tat gac cat g.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-684-215B-23 (1-128) x CB679186 (1-726)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.0761
120.50
44.03%
30.60%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                           JOURNAL
                                           REFERENCE
                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSJNEFOZF19.r OSJNEF Oryza sativa (japonica cultivar-group) cDNA clone OSJNEFOZF19 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 SerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerVal 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 TACGGCCTCGACAAGCCGTCCGGCGCTGGTGGCGCAACTGGTGGAAGACGGCCCGGCG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 AlaSerLeuGlyIleSerThrGlyAspValIleThrAlaValAspGlyAlaProlleAsn 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SerAspAsnPheGlnLeuSerGlnGly-----GlyGlnGlyPheAlalleProileGly 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 GlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHisIle 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 GTCGCGCTGAACGTCGCCGACCAGTTGAAGAAAGCCGGC------AAGGTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 ------GlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 GlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsn----------
                                                                                                                                                                                                                                                                                                                /clone="pacs1-60 1644"
/clone lib="pacs1-60"
note="clinical isolate 1-60 Whole genomic shotgun
                           õ
                           multiple isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                     959
40
21
24
5
                                                                                                                                                                                                                                1. .959
Organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="1-60"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                        Genome Center Mashington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Email: craymond@u.washington.edu
Class: shotgun:
       Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among researchanes arruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 ThrTrpGlnThrLysSerGlyGlyThr 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------GACGGGGATCC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-684-215B-23 (1-128) x BZ549048 (1-959)
                                                                                                                                                                                                                                                                                                   db_xref="taxon:287"
                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB679186.1 GI:29682911
                                                                                                                                                                                                                                                                                                                                                                                                                                    0.0809
122.00
47.29%
31.01%
18.74%
                                                                                                                                                                                                                                                                                                                                                                      library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
CB679186/c
                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
00
                                                         JOURNAL
                                                                                                                                                                                                                   FEATURES
                         TITLE
```

ò 임 δ 셤 ò 셤 ò g

Db

δ

ΩD

8

ò

97

68

```
/lab.host="burgarder" / lab.host="burgarder" 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              807 bp mRNA linear EST 25-SEP-2003 SCGGFL3058G06.g Saccharum officinarum FL3 Saccharum officinarum CDNA clone SCGGFL3058G06 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharum officinarum
Saccharum officinarum
Sucharum officinarum
Sucharum officinarum
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACCAD
Idae; Panicoideae; Andropogoneae; Saccharum.
(Dases 1 to 807)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
                                                                                                                                                                                                                                                                                               98 AlaLeuAsnGlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGly 117
                                                                                                                                                                                                                                           69 ProAlaAlaSerLeuGlyIleSer----Thr 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bccenter.fcav.unesp.br Plate: 058 row: G column: 06 Seq primer: T7 Promoter Primer.
29 GlnIleArgSerGlyGlyGlySerProThrValHisIleGlyProThrAlaPheLeuGly
                                                          66 AAAGITCGTGGTGCTGGCTTGAATGTGGACTTCGCTCCGGATCCAATTGCATAT----
                                                                                                                       49 LeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAla
                                                                                                                                                                                     120 -----cagctraatgrrcscaaccaaccacrraracrraagáraccrosscrst
                                                                                                                                                                                                                                                                                                                                                                             78 GlyAspValileThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .807
/organism="Saccharum officinarum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---ATCCGGCGAGGCTCAGAAACCCTT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 GlyThrArgThrGlyAsnValThrLeu 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCQGFL3058G06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: parruda@unicamp.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA228900.1 GI:35290878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
CA228900/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                          셤
                                                                                                                                                                       g
                                                                                                                                                                                                                                        . 첫 염
                                                                                                                                                                                                                                                                                                                                                                                 à
      à
                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /MOLE type="MRNA"
// Colliva=="MRNA"
// Colliva=="MRNA"
// Colliva=="MRNA"
// Colliva=="MRNA"
// Lone="MRNA"
// Lone="MRNA"
// Lone lib="Abscisic acid-treated seedlings"
// Clone lib="Abscisic acid-treated seedlings"
// Clone lib="Abscisic acid-treated seedlings"
// Clone lib="Abscisic acid-treated seedlings grown library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. After 12 days, medium was supplemented with a solution of 1 mM ABA. Roots and leaves were misted with a solution of 1 mM ABA. Roots and leaves were harvested after 3, 6, 12, and 24 hr and material from all time points was combined prior to RNA isolation.
Double-stranded cDNA was cloned unidirectionally into different Dralls sites of the pMR18S-F13 vector (5-prime Dralls site is CACCATGTGTG, 3-prime Dralls site is CACCATGTG). Xhol excises the cDNA insert."
                                                                                                                                                                                                                                                  Sorghum bicolor (sorghum)

Sorghum bicolor

Sorghum bicolor

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoddeae; Andropogoneae; Sorghum.

1 (Dases 1 to 590)

Cordonnier-Pratt, M. -M., Wentzel, V., Suzuki, Y., Sugano, S.,
Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Buchanan, C.D.,
Eastman, A., and Pratt, L.H.

An EST database from Sorghum: ABA1-treated seedlings
Unpublished (2003)
Other ESTS: ABA1_22 F06.91 A012
Contact: Cordonnier-Fratt M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mmpratreuga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bicinformatics,
university of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
                                                          CB925602
ABA1_22_F06.b1_A012 Abscisic acid-treated seedlings Sorghum bicolor CDNA_clone ABA1_22_F06_A012 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlypheAlaileProileGlyGlnAlaMetAlaileAla-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exclude polyA.
Seg primer: Sug3 (CGACCTGCAGCTCGAGCACA)
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .590
/organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-23 (1-128) x CB925602 (1-590)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                 CB925602.1 GI:30161873
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.112
117.50
44.19%
28.68%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
      RESULT 5
CB925602
LOCUS
                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ଟ
```

Ŋ

g ò g 8 유 ò g ठ g ò 셤 ò В

ð

```
/db_xref="taxon:375"
/lab_host="Es_col!"
/dlone_lib="B. japonicum BAC library"
/note="Vector: pindigo536; Site_1: HindIII"
                                                                                                      603
36
117
112
4
                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                      Length:
Matches:
                                                                                                                                                                         Gaps:
                                                                                                                                                                                                   US-09-684-215B-23 (1-128) x AZ934428 (1-603)
/strain="USDA110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ514888
BQ514888.1 GI:21373757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence
                                                                                                                  114.00
43.44%
29.51%
17.51%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrLeu 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCCTC 598
                                                                                                                                              Best Local Similarity:
Query Match:
                                                                                                                                 Percent Similarity:
                                                                                            Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                             82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               593
                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ514888/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                        No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                 ORIGIN
                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                    Ω
                                                                                                                                                                                                                                                                                                                                    8 8 8
                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                   જ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ914428 603 bp DNA linear GSS 24-APR-2001
By BaC002108r B. japonicum BAC library Bradyrhizobium japonicum
Genomic, genomic survey sequence.
AZ914428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobiaceas, Bradyrhizobium.

1 (bases 1 to 603)

1 (bases 1, P., Wood, T.C., Stacey, M.G., Loh, J.T., Judd, A.,
Goicoechea, J.L., Stacey, G., Sadowsky, M.J. and Wing, R.A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
                                                                                                                                                                                                                                285
                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                             77 ------ThrGlyAspValileThrAlaValAspGlyAlaProileAsnSerAla 92
                                                                                                                                                                                                                ------GlyGlnIleArgSerGlyGlyGlySerProThrValHisIleGlyPro 43
                                                                                                                                                                                                                                                                     44 ThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArg 63
                                                                                                                                                                                                                                                                                                                                                                                                                               93 ThralaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerValThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                     344 GGTAACATTGTTCTTGGTGATGTCATCGTTGCAGTGGATGGCAAACCTGTTAAGGGCAAA
                                                                                                                                                                                                                                                                                                                          64 ValValGlySerAlaProAlaAlaSerLeuGlyIleSer------------
                                                                                                                                                             SerGlnGlyGlyGlnGlyPheAlaileProlleGlyGlnAlaMetAlaileAla----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 GlnThrLysSerGlyGlyThrArgThrGlyAsnValThrLeu 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bradyrhizobium japonicum"
/mol_type="genomic DNA"
                                      807
38
20
47
47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Fax: 864 656 4293
Class: BAC ends
                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 11 (8), 1434-1440 (2001)
                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: BAC ends
High quality sequence stop: 553.
Location/Qualifiers
                                                                                                                                   US-09-684-215B-23 (1-128) x CA228900 (1-807)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ934428.1 GI:13776488
GSS.
                                      0.278
115.50
43.28%
28.36%
17.74%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .603
                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21376150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11483585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              депоше
                             Alignment Scores:
                                                                                                                                                               10
                                                                                                                                                                                                                   28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
AZ934428
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                         No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
  ORIGIN
```

```
Solanum tuberogum (potato)
Solanum tuberogum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Solanum tuberogum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
1 (Dases 1 to 758)
Solanales; Solanaceae; Solanum.
1 (Dases 1 to 758)
Sestrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
Karamycheva,S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002)
Other ESTS: EST622302
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-arrayedigr.org
Email: potato-arrayedigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ514888 17-MAR-2003 SET 07-MAR-2003 EST622303 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMIO81
                                                                                                                                                                                                                                                                                        415
                                                                                                                                                                                                                                                                                                                                                                                                     475
                                                                                                                                                                                                                                                                                                                                                                                                                                                            104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
                                    64
                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                33 GlyGly-------GlySerProThrValHisileGlyProThrAlaPheLeuGly 48
GlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleArgSer
                                                                                                                                                                                                                                                                     105 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 LeuGlyValValAspAsnAsnGly------AsnGlyAlaArgValGlnArgVal
                                                                                                                                                                       305 AAGGGTTCGGTCAGCCGCGGCTGGATCGGCGTGCAGTTCAGCCGGTGACG-----
```

Mon May 3 U6:36:19 200

```
Brasil
                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
BZ561390/c
LOCUS
DEFINITION I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                             .. oN
                                             JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \overset{\sim}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 챵
                   Schistosoma mansoni
Schistosoma mansoni
Schistosoma mansoni
Bukaryota, Metazoa Platyhelminthes; Trematoda; Digenea;
Striggidida; Schistosomatoidea; Schistosoma.

1 (bases 1 to 982)
Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M., Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M., Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,
Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,
Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,
Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD080132 989U-M294-C03-U.B MA3-0001 Schistosoma mansoni cDNA clone MA3-9999U-M294-C03.B, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                         ::: |||
532 TTGATCCAATCTGGAAAAGTTCTTCGTGCTGGTTTGAATATTGAAATCGCTCCAGACCTG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------ATTGCCAACCAACTTAATGTTCGAAATGGAGCACTGGTTTTGCTGGTACCT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAjaArgValGlnArgValVal 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94
                                                                                                                                                                                                                                                                                                                                                                         SerGlnGlyGlyGlyPheAlalleProlleGlyGlnAlaMetAlalleAlaGlyGln 29
                                                                                                                                                                                                                                                                                                                                                                                                                          30 IleargSerGlyGly------GlySerProThrValHisIleGlyProThrAla 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 ileserThrGlyAspValileThrAlaValAspGlyAlaProileAsnSerAlaThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlySerAlaProAlaAlaSerLeuGly------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 MetAlaAspAlaLeuAsnGlyHisHisProGlyAspVallle 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   758
115
118
3
                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                 US-09-684-215B-23 (1-128) x BQ514888 (1-758)
         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD080132.1 GI:34631128
                                                                                                                                                                                                                                                         0.449
113.00
42.98%
29.82%
17.36%
Seg primer:
                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
CD080132
             PEATURES
                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   рp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                           ઠે
```

```
BZ561390 1033 bp DNA linear GSS 17-DEC-2002 pacs2-164_3239.y3 pacs2-164 Pseudomonas aeruginosa genomic clone
Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C.C. and Dias-Neto, E. Transcriptome analysis of the accelomate human parasite Schistosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::|||:||
415 TICATACAGITAGCACTAAAAGCAICCTCAAATACTCGGAGCTCTTCCCCAAIATCGTCA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             475 AAATCGCCTAACTGACCCATATTTTAGCAGACAATCCAGCCAATTCGGAAAGTGGAACT 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :::|||||||||||||
535 CAACGICGAIACTIAGGCCTAGITAIGCGGACACITACICCAGAACIGGCITICGAAITA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------MetalalleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 ValAspAsnAsnGly-------AsnGlyAlaArgValGlnArgValVal 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Fax: +55-11-3091-2186
Faxi: +55-11-3091-2186
Fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------- 51yval 51
                                                                                                                                                                                                                                                                                                                                                                                               SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlySerAlaproplaAlaSerLeuGlyIleSerThrGlyAspVallleThrAlaValAsp
                                                                                                                                                             Nat. Genet. 35 (2), 148-157 (2003)
22879926
Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Dniversidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaileProlleGlyGlnAla-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 -----AlaPheLeuGlyLeu------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .982
/organism="Schistosoma mansoni"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xxef="xexon:6183"
/clone="mA3-9999U-M294-C03.B"
/sex="mixed pool"
/dev stage="adult"
/lab_host="Mus musculus"
/clone_lib="MA3-0001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-23 (1-128) x CD080132 (1-982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyalaProlleAsnSerAla 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTCTGCCTATAACGAATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.05
108.00
37.80%
25.98%
16.59%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 IleGlyProThr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
```

```
593 radaceradrantichesaastsaacaadantreseesasteiredeeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 laThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValileSerVal--- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            713 réceagritirécacegrécacedécrearesecergrerritésearitécariésar 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alAspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 erLeuGlyIleSerThrGlyAspValileThrAlaValAspGlyAlaProIleAsnSerA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 GlnAlaMetAlaile-AlaGlyGlnIleArg-----Se 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerAspAsnPheGlnLeuSerGlnGlyGlyGln-----GlyPheAlaileProileGly 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rGlyGlyGlyGlyBerProThrValHisIleGlyProThrAlaPhebeu-GlybeuGlyValV
                                                    Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas
1 (bases 1 to 1033)
                                                                                                                         Sims, E.E., Hastings, M.,
                                                                                                                                                                                                                                                                                                                   Spencer, D.H., Earwood, C.K., Smith, E.E., Sims, E.E., Hastings Burns, J.L., Kaul, R. and Olsen, M.V. Whole-Genome-Sequence variation among multiple isolates of Psedomonas acruginosa library J. Bacceriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 TGATTCGCAACGGCCAGCGCAAGTCCCTGAGCATGGCGGTAGGCAGCCTT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 -----ThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1033
20
20
20
21
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
pacs2-164_3239, genomic survey sequence.
BZ561390
BZ561390.1 GI:27181349
                                                                                                                                                                                                        Genome Center

Genome Center

Muschipty of Washington

Box 35145, Seattle, WA 98105-2145, USA

Tel: 2062216954

Email: craymond@u.washington.edu

Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-23 (1-128) x BZ561390 (1-1033)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.11
106.50
44.20%
29.71%
16.36%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
DB:
          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                               JOURNAL
                                                                                                             REFERENCE
                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

BZ549	047/c	
LOCUS	ITION	BZ549047 N pacel-60_1644.sl pacel-60 Pseudomonas aeruginosa genomic clone
0000	MOTO	pacs1-60_1644, genomic survey sequence.
VERSION	NO	BZ549047.1 GI:27152628
SOURCE		GSS. Pseudomonas aeruqinosa
ORG	NIS	
		Bacteria; Proteobacteria; Gammaproteobacteria; Fseudomonadales; Pseudomonadaceae; Pseudomonas.
REFERENCE		6 1 1
AUT		, stills, b.b., nascrings,
TILLE		Whole-Genome-Sequence variation among multiple isolates of
Jon	¥	J. Bacteriol. (2002) In press
COMMENT	IN	Contact: Chris K. Raymond
		nington
		Box 352145, Seattle, WA 98105-2145, USA
		Email: craymond@u.washington.edu
FEATURES	RES	i est
	source	1947 /ordanism="Dsendomonas aemidinosa"
		"genomic DNA"
		/strain="1-60" /aw6="t-20".207"
		/db_xrer="taxon:28/" /clone="pacs1-60 1644"
		-60"
		/note="clinical isolate L-60 Whole genomic Bhorgun library."
ORIGIN	×	
Alignment A		រ ពេក្ស ពេក្ស
Pred. No.	••	5.43 Length:
Score: Percen	: ent Sim	103.50 Macches: 3
Best	Local	Best Local Similarity: 32.46% Mismatches: 48
DB:		28 Gaps:
0-SD	9-684-2	-215B-23 (1-128) x BZ549047 (1-947)
δ ·		4 SerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaileProileGly 21
q	м	
Š		22 GlnalaMetalaTlealaGlvGlnTleArgSer32
ŝ		
셤	m	314 GTCGCGATGAACGTCGCCGACCAGTTGAAGAAAGCCGGCAAGGTCAGTCGCGGCTGGCT
à		33 GlyGlyGlySerProThrValHisIleGlyProThrAlaPheLeuGlyLeuGlyValVal 52
Q	7	254 GGCGT-GGTGATCCAGGAAGTGAACAACGATCTCGCCGAGTCTTCGGCCTC 205
ò		53 AspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSer 72
qq	N	::: ::: ::: ::::::::::::::::::::::::::
ò		73 LeuGlylleSerThrGlyAspVallleThrAlaValAspGlyAlaProlleAsnSerAla 92
Ωp	н	147 GGTGGCCTGCAGGTGGGCGATGTGACAGCCTGAACGGCCAGTCGATCAACGAGTCC 88
δŏ		93 ThralaMetalaAspalaLeuAsnGlyHisHisProGlyAsp 106
q		::: 87 GCCGACCTGCCGCACCTGGTGGAACATGAAGCCGGGCGAC 46
RESULT	LT 12	-

AQ989479

BZ549047/c LOCUS DEFINITION

```
셤
                                                                                                                                                                                                                                                                                                                                                         Contact: ffrench-Constant RH
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bestfc@bath.ac.uk
This is one of 2.122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTX and mapping to B.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
Location.Qualifiers
1. 726
/organism="Photorhabdus luminescens"
/strain="W14"
      14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 CTTCAAGGGCTACGAGTATTTCAGGTAACTACAAAGGGGCCTGCGCAAAAAGCCGGTATT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :::|||
179 TCATTCGATAAAAGTGAAAATGGTGAAACGCCAGAAGGGTTGGGGTTCGCTATTCCGACT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 Arceccarakcarcecaagagcreccacararrecererrerakceccaararaaccag 358
                                                                                                                                                                                                    1 (bases 1 to 70.0.)
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 -----GlyalaargyalGlnargyalvalGlySeralaProalaalaSerLeuGlyile 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerThrGlyAspValIleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMet 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 AsnPheGlnLeuSerGlnGlyGlyGlyGln------GlyPheAlaileProIle 20
                                                                                                                                      Photorhabdus luminescens
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
AQ989479 14-AUG-:
Rfc00025 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00025, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsn-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:29488"
/clone="PLG00025"
/dev stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       726
39
115
52
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-23 (1-128) x AQ989479 (1-726)
                                                                              AQ989479.1 GI:9648073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.14
103.00
46.55%
33.62%
15.82%
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Si
Query Match:
DB:
                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Мо.:
      LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                  MEDLINE
PUBMED
COMMENT
                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
DNA linear GSS 24-APR-2001 BJ Ba0001B03r B. japonicum BAC library Bradyrhizobium japonicum AZ933900
                                                                                                                   Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bacteria, Proteobacteria, Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.

1 (bases 1 to 719)

1 (bases 1, P., Wood, F.C., Stacey, M.G., Loh, J.T., Judd, A.,
Goicoechea, J.L., Stacey, G., Sadowsky, M.G. and Wing, R.A.

A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 GGCGGCAAGGCGGTGAAGCGTCCCTGGCTCGGCGGAAGTTGCAGGCGGTGACGCCGAG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValileThrAlaVal 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 GlyGlnGlyPheAlaileProlleGlyGlnAlaMetAlaileAlaGlyGlnIleArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 GlyGly-----GlySerProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / 1. 179
/ organism="Bradyrhizobium japonicum"
/ mollen="Bradyrhizobium japonicum"
/ strain="USDA110"
/ db xref="taxon:375"
/ lab host="E. coli"
/ clone lib="B. japonicum BAC library"
/ note="Vector: pindigo536; Site_1: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute Clemson University 1100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Class: BAC ends
                                                                                                                                                                                                                                                       genome
Genome Res. 11 (8), 1434-1440 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215B-23 (1-128) x AZ933900 (1-719)
                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 671.
Location/Qualifiers
                                                                                    AZ933900.1 GI:13775960
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.13
102.00
44.44%
28.89%
15.67%
                                                                                                                                                                                                                                                                                                 11483585
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                           DEFINITION
                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                 MEDLINE
PUBMED
COMMENT
                                                                                                                                                                                       REFERENCE
AUTHORS
RESULT 13
AZ933900
LOCUS
                                                                             ACCESSION
                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \dot{\delta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
```

419 AAAGIGGGIGATATCATTACCAGGGTCAATAACAAACCCGCTATTCTGCGGGTGAAACA 478

96 AlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerValThr 111

AGENCOURT 10739220 NCI_CGAP_ZEmb2 Danio rerio cDNA clone IMAGE:6789351 5', mRNA sequence. 66 Query Match: VERSION KEYWORDS SOURCE ORGANISM . У DEFINITION REFERENCE AUTHORS TITLE JOURNAL COMMENT ACCESSION FEATURES ORIGIN 셤 ઠે 8 8 8 ઠ g ઢ g ઇ 765 bp mRNA linear EST 12-JUN-2003 AJ558965 Antirrhinum majus whole plant Antirrhinum majus cDNA clone AJ588965 EST 13-NOV-2002 AJ558965.1 GI:31661537
BEST.
BEST.
Antirrhinum majus
Antirrhinum majus
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamiids, Lamiales, Antirrhinaceae, Antirrhineae;
Antirrhinum. 583 IleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIle 108 1 (bases 1 to 765)
Zachgo,S., Stueber,K., Saedler,H., Sommer,H. and Schwarz-Sommer,Z. Antirrhinum EST collection
Unpublished (2003)
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Meg 10, D-50829, Germany.
Location/Qualifiers 371 TTG----------ATCAATTATGGAAAGTTGTTGGAGCTGGTTA 407 AAT----GITGACATAGCTCCTGATCTTTGCAAATCAACTCAAHGTTCGAAATGAAGCT 463 523 5 88 30 IleArgSerGlyGlyGlySerProThrValHisIleGlyProThrAlaPheLeuGlyLeu 49 60 ArgvalGlnArgvalValGlySerAlaProAlaAlaSerLeuGly------74 SerGlnGlyGlyGlnGlyPheAlaIleProlleGlyGlnAlaMetAlaIleAlaGlyGln 29 464 CTAATCTTGCAGGTCCCTGGAAATAGTTCAGCAGCTAAGGCTGGGCTTGTACCTACAACA -----IleSerThrGlyAspValileThrAlaValAspGlyAlaPro 524 CGGGGTTTCGCTGGTAAATCGTACTTGGGGATATATTTTGGCCGTAGATGACAAACCT -----AsnAsnGlyAsnGlyAla /clone="018 1 09 a08" /tissue type="whole plant" /clone_lib="Antirrhinum majus whole plant" linear Length:
Matches:
Conservative:
Mismatches:
Indels: **MRNA** 1. 765 /organism="Antirrhinum majus" /mol_type="mRNA" /db_xref="taxon:4151" 85 AspGlyAlaProlleAsnSerAlaThrAla 94 Gaps: (1-765)ď 50 GlyvalvalAsp------859 US-09-684-215B-23 (1-128) x AJ558965 5.61 102.00 40.83% 28.33% 15.67% 75 -----Percent Similarity: Best Local Similarity: CA480614 Alignment Scores: 10 278 Query Match: DB: RESULT 14 AJ558965 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM RESULT 15 CA480614/c LOCUS Pred. No.: REFERENCE AUTHORS TITLE JOURNAL COMMENT ACCESSION FEATURES ORIGIN ò 셤 ò g δ d ð g ò 셤 ò g 8

```
SERT.
Danio rerio (zebrafish)

[ISM Danio rerio (zebrafish)

[ISM Danio rerio Danio rerio (zebrafish)

[ISM Danio rerio
Danio rerio
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

[Cypriniformes: Cyprinidae; Danio.

[Cypriniformes: Leonard In. Gov.

[Contact: Robert Strausberg, Ph. D.

[Email: Ggapbs-r@mail.nih.gov.

[Contact: Robert Strausberg, Ph. D.

[Email: Ggapbs-r@mail.nih.gov.

[Contact: Robert Strausberg, Ph. D.

[Contact: Robert Strausberg, Ph. D.

[Email: Ggapbs-r@mail.nih.gov.

[Contact: Robert Strausberg, Ph. D.

[Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="embryo"
/lab hose="bH108 (T1-resistant)"
/clone_lib="NOT_GAP_ZEMb2"
/note="bH108 (T1-resistant)"
/note="bH108 (T1-resistant)"
/note="bH108 (T1-resistant)"
/note="bH108 (T1-resistant)
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeudanGlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGly 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TTC 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    592 CCTCTCAGCTGTGGTGGTGAAGCTGTAGCCTCTCTCGGTCAGGATCTTCATGAGGTAGTC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 GlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        532 AGTCAGGTCACGCCAAGCCAAGTCCAGACGGAGGATGGCATGGCATGGGCAGGGCAGGGCTAACCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 ThralavalaspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAla-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 GlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 SerGlnGlyGlyGlnGlyPheAlalleProlleGlyGlnAlaMetAlalle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 AlaGlyGlnIleArgSerGlyGlyGlySerProThrValHisIle---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                734 geccacaraecaeaecircrecricarerereeaeaear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   859
36
18
55
55
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:6789351"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-23 (1-128) x CA480614 (1-859)
CA480614.1 GI:24938284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.36
100.50
40.30%
26.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.44%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores
```

us-09-684-215b-23.rst

```
43 ProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGln 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:4955073"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                             345 ACCCCTTCTGGG 356
                                                                                                                                                                                                                                                                        119 ThrargThrely 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   воитсе
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                       LOCUS
                                                                                                                                                                                                                                                                                                                                          RESULT 17
BI350520/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                 දු දු
                                                                                                                                                                                                                                                                                                셤
               g 8
                                                                   8 8
                                                                                                                                         Š
                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. and Denaldo, Ph.D. con Edward Arrayed by: Greg Lennon, Ph.D. con Library Arrayed by: Greg Lennon, Ph.D. con Edward Arrayed by: Greg Lennon, Ph.D. Sequencing by: Washington University Genome Sequencing by: Washington University Genome Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
Seq primer: -40UP from Gibco.
                                                                                                                           AIS97611 423 bp mRNA linear EST 21-APR-1999 tn15f02.xl NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2167707 3' similar to TR:008664 O08664 BCL7C MRNA.;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAGGGGCATTTGGGCAGATGCGCTTGAGTGGGGGGGGCACCCTCCAAGTCCTTTGTGTCA 158
                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 MetalallealaglyGinIleargSerGlyGlyGlySerProThr --- ValHisIleGly 42
Eukaryogia.

Bukaryogia.

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Mori/NINDS-CaAP http://www.ncbi.nlm.nih.gov/ncicgap.

Nci/NINDS-CaAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/PRTGAP), Tumor Gene Index

Unpublished (1998)

Contact: Robert Straubberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 PheGlnLeuSerGln-----GlyGlyGlnGlyPheAlaIleProIleGlyGlnAla 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 TTTGAAAAAAGCCAAAAGGGGCCCCTGGGGCAACAGGACAGGCCAGGCCGGTTTCTCAGGGG 98
                                                              512 ACCAGAGGCATACAGGGACAGCACAGCCTGGATGGCAACGTA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453
35
45
72
72
72
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-23 (1-128) x AI597611 (1-423)
                                                                                                                                                                             AIS97611
AIS97611.1 GI:4606659
                                                                                                                                                                                                             EST.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.71
99.00
44.35%
28.23%
15.21%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                 119
                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                             RESULT 16
AI597611
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . No.:
                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
 g
                               ò
                                                                g
```

```
Eukaryota, Metazoa; Chordata, Cramiata; Vertebrata; Euteleostomi; Actinopteryoti; Neopteryoti; Teleostei; Ostariophysi; Cyprinidae; Danio.

Actinopteryoti; Neopteryoti; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

Cypriniformes; Cyprinidae; Danio.

Cypriniformes; Cyprinidae; Danio.

RS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Clark,M., Johnson,S.L., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Riter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Rathor, E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Mashu Zebrafish Est Project 1998

LUpublished (1998)

Lupublished 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499 bp mRNA linear EST 26-JUL-2002 IMAGE:4955073 5' similar to SW:ACT2_FUGRU P53485 ACTIN, CYTOPLASMIC B1350520 GI:15044966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 TAAGCTICGGGGCCTCACCTICCAGCAGTCTGGA-----ACAGGCTCCTCCTTGGTC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 AlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 102
                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="mixed male and female"
/tissue_type="brain"
/tissue_type="brain"
/lab_host="E. coli DH10B"
/clone_lib="zebrafish adult brain"
/clone_lib="zebrafish adult brain"
/clone="brain"
/clo
63 ArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVallleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .499
/organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Www.rgu.cc,
Seq primer: T7
High quality sequence stop: 301.
Location/Qualifiers
```

ò

 $\stackrel{>}{\circ}$

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Pukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi; Cypriniformes; Cyprinidae, Danio.

1 (Dases 1 to 870)

S NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
EDmail: Gaphys-remail.nih.gov

Tissue Procurement: Leonard I. Zon, M.D.

CONTACT: Robert Strauberg, Ph.D.
DNA Library Preparation: Invitrogen Corp.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linl at:

High quality sequence stop: 671.

High quality sequence stop: 671. CA473840

AGENCOURT 10740457 NCI_CGAP_ZKidl Danio rerio cDNA clone
IMAGE:6794807 5', mRNA sequence.
CA473840.
CA473840.1 GI:24930192
EST.
BST.
Danio rerio (zebrafish) 217 GATCTTCATGAGGTAGTCAGGTCAGGTCAGCCCAGGCCAGGTCCAGAGGATGGCATG 158 96 AlaAspAla-----LeuAsnGlyHisHisProGlyAspValIleSerValThrTrp 112 GlnThrLysSerglyGlyThrArg------ThrGlyAsnVal 124 430 checarchececrerecaecacereraacerrecearrecearcereaecererecere 371 319 CTCCTGCTCAAAGTCAAGGGCCACATAGCAGAGCTTCTCCTTGATGTCACGACAAT--- 263 157 GGGCAGGCGTAACCCTCGTAGATGGGCACAGTGTGGGTGACACCATCACCATAGTCCAT 98 41 Ile-------GlyProThrAlaPheLeuGlyValValAspAsnAsn 55 56 GlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIle 75 76 SerThrGlyAspVallleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMet 95 CACGATACCAGTGGTACGACCAGAGGCATACAGGAACAGCACAGCCTGGATGGCAACGTG 38 ----GlyGlnGlyPheAlalleProlle 20 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40 excision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library." Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-09-684-215B-23 (1-128) x BI350520 (1-499) 9 LeuSerGlnGly-----8.44 97.50 39.29% 27.14% 14.98% Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: Scores: 6 ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS RESULT 18 CA473840/c REFERENCE AUTHORS TITLE JOURNAL COMMENT Alignment & Pred. No.: FEATURES ORIGIN g d ò a ò qq ઠે 셤 à 원 ò g

source

```
CA148171
SCEZEZIO17F10.g RZ1 Saccharum officinarum cDNA clone SCEZEZIO17F10
5', mRNA sequence.
CA148171
GA148171 GI:35048941
BST.
/organism="Danio rerio"
/wol_type="mRNA"
/db xref="taxon:7955"
/db xref="taxon:7955"
/dlone lib="NGI GGAP_ZXid"
/lab_host="DH10B (T1-resistant)"
/dlone lib="NGI GGAP_ZXid"
/note="Organ: kIdney, Vector: pCMV-SPORT6.1; Site 1:
Rocky; Site 2: Not1; Cloned unidirectionally. Primer:
Coligo dT. Average insert size 1:8 kb. Constructed by J.
Wang (Research Genetics, Invitrogen Corp) from tissue
donated by L. Zon (Harvard University). Note: this is a
NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Streptophyta, Embryophyta,
Sapermatelophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Pantcoideae, Andropsoneae, Saccharum.
1 (bases 1 to 444)
Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 ProlleAsnSerAlaThrAlaMetAlaAspAla-----LeuAsnGlyHisHisPro 104
                                                                                                                                                                                                                                                                                                                                                                                                                    16 PheAlaileProileGlyGlnAlaMetAlaile-----AlaGlyGlnIleArgSer 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 GlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySer 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::: ::: ||||||||
589 CAAGTCCAGAAGATGGATGGCATGGGGCAGGGCGTAACCCTCGTAGATGGGCAAGGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 GlyGlyGlySerProThrValHisIle-------GlyProThrAlaPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TICCCICICAGCIGIGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
                                                                                                                                                                                                                                                                  870
117
251
551
                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-23 (1-128) x CA473840 (1-870)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               səı crecingandicacgdacaar-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ThrGlyAsnVal 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469 CAGCACAGCCTGGATGCCAACGTA 446
                                                                                                                                                                                                                                                                  18.9
97.50
40.62%
27.34%
14.98%
                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                     Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA148171
                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ठ
```

us-09-684-215b-23.rst

```
Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br

Plate: 017 row: F column: 10

Seq primer: 77 Proncer Primer.

Location/Qualifiers
                                                                                         FEATURES
```

444 444 444 148 264 264 Length:
Matches:
Conservative:
Mismatches:
Indels: 7.99 97.00 47.62% 30.95% 14.90% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores:

US-09-684-215B-23 (1-128) x CA148171 (1-444)

103 HisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGly 122 -----ATCCGGCGAGGC 250 |||:::::: |GCCTTGCTCCGACCGGCAGGGTTTCGCTGGTAACATTGTTCTTGGTGATGTCATCGTT 151 83 AlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 102 91 82 54 AsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeu 73 123 AsnValThrLeu 126 92 152 g 8 & ò g δ В Š ò

543 bp mRNA linear EST 19-SEP-2001 L031054B10.yl C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence. B1721127.1 GI:15696822 EST. RESULT 20 BI721127 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Chlamydomonas reinhardtii Chlamydomonas reinhardtii Bukaryota, Viridplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas. 1 (bases 1 to 543) Grossman, A., Chang, C.-W., Davies, J., Harris, B., Hauser, C.,

REFERENCE AUTHORS

Fax: 919 613 8177

Email: chauser@duke.edu.

Location/Qualifiers

1. .543

| Location/Qualifiers
| Location/Qualifiers
| Location/Qualifiers
| Location/Qualifiers
| Location/Qualifiers
| Location | Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031
Unpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 277098-1000
Tel: 919 613 8159
Fax: 919 613 8177 JOURNAL FEATURES TITLE

Length:
Matches:
Conservative:
Mismatches:
Indels: 10.7 97.00 39.83% 26.27% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: Pred. No.:

ORIGIN

US-09-684-215B-23 (1-128) x BI721127 (1-543)

10 SerGlnGlyGlyGlyGlyPheAlalleProileGlyGlnAlaMetAlalleAlaGlyGln 29 30 ileargserGlyGly-----SerproThrvalHislleGly------proThr 44 à g δ 셤

318 CCCAAGGGCTCCCCCGCGGAGAAGGCCGGCATCAAGCCCACCATGCGCGACCGCTTCAGC 377

셤 ò

g 8

õ

93 ThralaMetalaAspalaLeuAsnGlyHisHisProGlyAspValIleSerVal 110

us-09-684-215b-23.rst

```
Sorghum bicolor (sorghum)

Sorghum bicolor (sorghum)

Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

El (bases 1 to 551)

Cordonnier-Pratt, M.-M., Gingle, A., Mareala, C. and Fratt, L.H.

An EST database from Sorghum: light-grown seedlings

th Chipublished (2000)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions

below, Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .551
/moltype="mcNaphum bicolor"
/moltype="mcNaphu"
/db_xref="taxon:4558"
/db_xref="taxon:4558"
/dolone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2:
secallings; Vector: Lambda Zap; Site_1: XhoI; Site_2:
vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."
LG1_241_G05.g1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA sequence.
AW285527
AW285527.1 GI:6675371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 AlayalaggiyalaprolleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ATCCGGCGAGGC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 AsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeu 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 HisProglyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 GlyileSer-----ThrGlyAspValileThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251
251
26
26
26
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GGCGTCGGAGATCAGGTGACCTTGACA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-23 (1-128) x AW285527 (1-551)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7
High quality sequence start: 16
High quality sequence stop: 552
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.7
96.00
47.62%
29.76%
14.75%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 AsnValThrieu 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGAAGCCTT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
DB:
RESULT 22
AW285527
LOCUS
DEFINITION
                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ک</u> ۾
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              & B
                                                                                                                                                                     Sorghum bicolor (sorghum)
SM Sorghum bicolor

Sw Sorghum bicolor

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

El (basses I to 546)
Cordonnier-Pratt,M.-M. Gingle,A., Marsala,C. and Pratt,L.H.
An EST database from Sorghum: light-grown seedlings
L (phypulished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 1546
1. 154
        AWZES510 546 bp mRNA linear EST 19-JUL-2000
LG1 241_E05.g1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 HisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGly 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||::::::
||||||::::|||
| GGTCTTGCTCCAACCGGCAGGGGTTTTGCTGGTAATAITGTTCTGGGTGATGATGATCGTT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 AlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmprattenga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ATCCGGCGAGGC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 AsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeu 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ThrGlyAspValileThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2546
115
118
26
27
27
27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||||||
236 GGCGTCGGAGATCAGGTGACCTTGACA-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: T7
High quality sequence start: 126
High quality sequence stop: 546
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-684-215B-23 (1-128) x AW285510 (1-546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                         AW285510
AW285510.1 GI:6675354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlylleSer------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.5
96.00
47.62%
29.76%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 AsnValThrLeu 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 TCAGAAACCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
  AW285510
LOCUS
DEFINITION
                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \dot{\delta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

122

```
203 GGTGACGTCATCACCAGTATCAACGGTCGATAGGTGACGTCAGCACGAGACATCTACGAC 262
                                                   58 GlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThr 77
                                                                                                             143 GGAGTACTGGGGATCATTGTGGGGTCACCTGCATACAGTGCGGGTATCCGTCCT
                                                                                                                                                                             78 GlyAspValileThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAsp
                                                                                                                                                                                                                                                                                                                                    263 GCGGTAAATAGC-----GGGCAGCAGCAGCTGAACATCACC 295
                                                                                                                                                                                                                                                                                                    98 AlaLeuAsnGlyHisHisProGlyAspValileSerValThr 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    909
38
117
55
58
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-23 (1-128) x CA975497 (1-909)
US-09-684-215B-23 (1-128) x BI378928 (1-677)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA975497
CA975497.1 GI:27508151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST.
Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.7
95.00
39.86%
27.54%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 24
CA975497/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                   음
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                슝
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Panopoulou G
laboratory 145, dept.Lehrach
laboratory 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Inhestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1228
Email: panopoul@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
Toredure, clones giving the same hybridisation pattern with a
battery of 200 Bear oligonucleotides are grouped into clusters. One
clone per cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well the coordinates of the
rest of the clones assigned to the same fingerprint cluster as the
clone from which the above EST is generated is available ar the
amphioxus project site at: http://www.nolgen.mg/dc/amphioxus/
Clones and filters are distributed via the Resource Center/Primary
Database of the German Genome Project (http://www.rzpd.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .677
| organism="Branchiostoma floridae" |
| organism="Branchiostoma floridae" |
| mol_type="mkla" |
| db xref="taxon:7739" |
| clone="MPMGp498P1235" |
| flishee_type="whole embryo" |
| dev stage="5-6 hrs (gastula stage)" |
| lab_host="E.coli, XLI blue" |
| lab_host="5-6 hrs (gastula stage)" |
| lab_host="6-6 hrs (gastula stage)" |
| lab_host="6-6 hrs (stage)" |
| lab_host="6-6" |
| lab_ho
                                                            EST 26-AUG-2003
                                                      BI378928
BFLG1 000559 Amphioxus 5-6 hrs cDNA library (Name convention: BFLG or MPMGp498) Branchiostoma floridae cDNA clone MPMGp498P1235 5',
                                                                                                                                                                                                                                                                   Branchiostoma floridae (Florida lancelet)
Branchiostoma floridae
Eukaryota, Metazoa, Chordata, Cephalochordata, Branchiostomidae,
                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 677)
Panopoulou, G., Hennig, S., Groth, D., Krause, A., Poustka, A.J., Pearogoulou, G., Hennig, S., Groth, D., Krause, A., Vingron, M. and Lehrach, H.
New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP)
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP)
Insert Length: 1200 Std Brior: 0.00
Seq primer: 5'-CCGTCCGGAATTCCGGGT-3' pSport3/86
High quality sequence stop: 677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           677
21
12
18
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 13 (6A), 1056-1066 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                          BI378928.1 GI:30914099
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.7
95.50
61.11%
38.89%
14.67%
                                                                                                                                                      sednence.
                                                                                                                                                                                                                                                                                                                                                                 Branchiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22683279
                                                                                                                                                                             BI378928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                      BI378928
LOCUS
DEFINITION
                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
MEDLINE
PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
   RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (Dases 1 to 903)

1 (Dases 1 to 903)

2 National Institutes of Health, Mammalian Gene Collection (MGC)

3 National Institutes of Health, Mammalian Gene Collection (MGC)

4 Unpublished (1999)

4 Contact: Robert Strausberg, Ph.D.

5 Email: Gappa-remail.nih.gov

7 Tissue Procurement: Leonard I. Zon, M.D.

5 CDNA Library Preparation: Invitrogen Corp.

5 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

5 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

6 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

8 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

8 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

8 CONDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

8 CONDA Library Arrayed by: The I.M.A.G.E. CONSORTIUM (LLNL)

8 CONDA Library Arrayed by: The I.M.A.G.E. CONSORTIUM (LLNL)

8 CONDA Library Arrayed by: The I.M.A.G.E. CONSORTIUM (LLNL)

8 CONS
CA975497 909 bp mRNA linear EST 06-JAN-2003 AGENCOURT 11067943 NCI_CGAP_ZKidl Danio rerio cDNA clone IMAGE:6805289 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LeuSerGinGiyGlyGlnGly-----PheAlaIleProIleGlyGlnAlaMetAla 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone=Indags:6805289"
/lab host="Indags:6805289"
/lab host="Indags:6805289"
/clone lib="NCI CGAP ZKidl"
/clone lib="NCI CGAP ZKidl"
/note="organ: kidney; Vector: pCNV-SPORT6.1; Site_1:
BCORV; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.8 kb. Constructed by J. Wang (Research Genetics, Invitrogen Corp) from tissue donated by L. Zon (Harvard University). Note: this is a NCI_CGAP Library."
```

```
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed from embryos representing early developmental stages
Upplication of 2003
Contact: Smith Tp.
USDA, ARS, US Meat Animal Research Center
Po Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329:
Plate: TWM8001 row: I column: 11
Seq primer: GTAATACGACTCACTATAGGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 21-OCT-2003
                                                                                                                                                                                                                    638
                                                                                                                                                                                                                                                                                                                                                                587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                467
                                                                 748 GTCAGGCAGCTCGTAGCTCTTCTCCAGGGAGGAGGAAGCAGCGGGGGCCCATCTCCTG 689
                                                                                                                                                                                                                                                                                      77
26 Ile-----AlaGlyGlnIleArgSerGlyGlyGlyGsrProThrValHisIle--- 41
                                                                                                                                                                                                                                                                                                                                                                                                                                         97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
1 (bases 1 to 600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa"
//mol_type="mRNA"
//db_xref="texon:9823"
//db_bost="DHIOB"
//lab_host="DHIOB"
//lab_host="DHIOB"
//lab_host="texon"
//lab_h
                                                                                                                                               42 -------GlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsn
                                                                                                                                                                                                                                                                                          58 GlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThr
                                                                                                                                                                                                                                                                                                                                                                637 -----TTCCCTCTCAGCTGTGGTGAAGCTGTAGCCTCTCTCGGTCAGGATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyAspValIleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 Ala ------LeuAsnGlyHisHisProGlyAspValIleSerValThrTrpGlnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       526 GGCGTAACCCTCGTAGATGGGGCACAGTGTGGGTGACCATCACCATCACGAT
                                                                                                                                                                                                             88 CTCAAAGTCAAGGGCCACATAGCAGAGCTTCTCCTTGATGTCACGGACAAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 LysSerGlyGlyThrArg------ThrGlyAsnVal 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 ACCAGTGGTACGACCAGAGCCATACAGGGACAGCCACAGCCTGGATGGCAACGTA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600 bp mRNA linear
854999 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
CF787130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 800
820
820
823
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF787130.1 GI:37791691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.9
94.50
44.83%
27.59%
14.52%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 25
CF787130/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOUNCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                      a
                                                                                                                                           ò
                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
1...647
| organism="Suns scrofa"
| organism="Suns scrofa"
| db xref="taxon:9823"
| clone="scac0037i.j.05"
| fissue type="mixed"
| fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 28-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 --------GGCACTGGCTCAAAGACGGGGTAAGCTTCAGGGGCCTCAGCCTCC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389 AGCAATTCTGGA-----ACAGGCTCCTCCTTGGTCAGCATCGGGGGTTCATCCTGCCG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 SerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerVal 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 CCTĠĊÁ-------rċdiATGCCCĊĆÁĠĠÁ-----rċdiCTC 309
                                                                                                                                                                                                                                       554 decenaración de consecuencia de contrator de contrador de contrado
                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 ValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAla 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.ina.fr
Email: tosser@toulouse.ina.fr
Clone distribution: AGENAE Resource centre. Francois PIUMI,
Francois.Plumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du
genome (LREG), Domaine de Vilvertr, 7885.2, Jouy-en-Josas cedex,
FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 AlaSerLeuGlyIleSerThrGlyAspValIleThrAlaValAspGlyAlaProIleAsn 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 647)
                                                                                                                       12 GlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleArg
                                                                                                                                                                                                                                                                                                                                                              32 SerGlyGlyGlySerProThrVal ---HisIleGlyProThrAlaPheLeuGlyLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villeger, S. Soares, M., Bonaldo, F. and Hatey, F.
A Pig Normalised Multi-Tissue cDNA Library Unpublished (2003)
Contact: Tosser-Klopp G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX674871 Sus Scrofa library (scac) Sus scrofa cDNA clone scac00371.j.05 5prim, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 ThrirpGlnThr-------bysSerGlyGlyThrArgThrGly 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 TCCTGGCCCAGCTGTGGGGGCTGAGCATCCTCAGGGACCCCTTCCGGT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: 0037, row: j column: 5.
Location/Qualifiers
US-09-684-215B-23 (1-128) x CF787130 (1-600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BX674871
BX674871.1 GI:38008823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cedex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 26
BX674871/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                       ò
                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
```

Alignment Pred. No	Percent Percent Description Main DB: US-09-68	S 6	ે દે	3 & £	3 8 8	ે જે તે	કે ઠે દે	8 & A	RESULT 2 CC345457 LOCUS DEFINITI	ACCESSIC VERSION KEYWORDS SOURCE ORGANI	REPERENC AUTHOI	TITLE JOURNY COMMENT	PEATURE	
epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder" ORIGIN	Alignment Scores: 24.4 Length: 647 Pred. No.: 94.50 Matches: 32 Score: 44.83\$ Conservative: 20 Best Local Similarity: 27.59\$ Mismatches: 41 Query Match: 14.52\$ Indels: 23 DB:	US-09-684-215B-23 (1-128) x BX674871 (1-647)	Qy 12 GlyGlyGlnGlyPheAlaileProileGlyGlnAlaMetAlaileAlaGlyGlnIleArg 31	Qy 32 SerGlyGlyGlyGerProThrValHislleGlyProThrAlaPheLeuGlyLeuGly 50	Qy 51 ValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAla 70	Qy 71 AlaSerLeuGlyIleSerThrGlyAspVallleThrAlaValAspGlyAlaProlleAsn 90	Qy 91 SerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerVal 110	Qy 111 ThrTrpGlnThrbysSerGlyGlyThrargThrGly 122 	RESULT 27 BJ285991/c LOCUS BJ285991 Coihara unpublished cDNA library, Wh_r Triticum aestivum cDNA clone whrl3124 3', mRNA sequence.	ACCESSION B1285991.1 GI:20105650 VERNONS EST. SOURCE Triticum aestivum (bread wheat) ORGANISM Triticum aestivum (bread wheat) Evkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	REFERENCE 1 (James 1 to 728) AUTHORS Oghhara,Y. and Murai,K. JITLE Expressed genes in Triticum aestivum JONENAL Unpublished (2002)	COMMENT Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856	Email: tshini@genes.nig.ac.jp. FEATURES Location/Qualifiers 1. 728 1. 728 Anganism="Triticum aestivum" mol.type="mRNA" cultivar="Chinese Spring" clone="Whrilla" / tissue type="root" / tissue type="root"	/dev_stage="Feekes" scale 1" /clone_lib="Y. Ogihara unpublished cDNA library, Wh_r"

g ò g g ઠે d

ò

셤

ઠે

```
Length:
Matches:
Conservative:
Mismatches:
Indels:
   lab host="DH10B (T1-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          727 ATAGCAGAGCÍTCTCCTTGATGTCACGGACAAT----
                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                     (1-907)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF265501
AGENCOURT 15130858 NIH_ZGC_7
5', mkNa Sequence.
CF265501
CF265501. GI:33605880
                                                                                                                                                                                                                                                                                                       US-09-684-215B-23 (1-128) x CA471201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                   Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF265501/c
                                                                                                                                                                                      ..
No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 30
                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 907)

1 (bases 1 to 907)

1 NH-MGC http://mgc.nci.nih.gov/.

1 National Institutes of Health, Mammalian Gene Collection (MGC)

1 Unpublished (1999)

2 Contact: Robert Strausberg, Ph.D.

2 Email: Gapba-remail.nih.gov/

1 Ssue Procurement: Leonard I. Zon, M.D.

2 CDNA Library Preparation: Invitrogen Corp.

2 CDNA Library Preparation: Invitrogen Corp.

3 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

5 DNA Sequencing by: Agencourt Bioscience Corporation

6 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

8 Plate: LLAM14294 row.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       907 bp mRNA linear EST 12-NOV-2002 AGENCOURT 10698245 NCI_CGAP_ZKidl Danio rerio cDNA clone IMAGE:6791062 5', mRNA sequence.
                                                                                                                                                                                                                                                                              473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            593
                                                                                                                                                                                                                                                                                                                                                     363 GATGGCCGGGTGATCCGCGGTTATATCGGTATTACC------GGCGCGCGAGCTGCCG 413
                                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                     13 GlyGlnGlyPheAlaileProileGlyGlnAlaMetAlaileAlaGlyGlnIleArgSer 32
                                                                                                                                                                                                                                                                                                                                                                                                             85 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                       33 GlyGlyGlySerProThrValHisIleGlyProThrAlaPheLeuGlyLeuGlyValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 ----SerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
/clone_lib="ZM_0.7_1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic_DNA_library"
                                                                                                                                                                                                                                                                                                                                                                                       53 AspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGly-----
                                                                                                600
32
10
110
2
                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .907
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:6791062"
                                                                                                                                                                                                                     US-09-684-215B-23 (1-128) x CC345457 (1-600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 590.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA471201.1 GI:24927553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danio rerio (zebrafish)
Danio rerio
                                                                                              27.5
93.50
41.58%
31.68%
28
                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 Gly 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              594 GGA 596
                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST.
                                                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 29
CA471201/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
DEFINITION
                                                                                                    No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
```

```
bp mRNA linear EST 12-AUG-2003
Danio rerio cDNA clone IMAGE:6996778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 valAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAla------LeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

Cypriniformes; Cyprinidae; Danio.

I (bases 1 to 913)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Len Zon, Harvard

CDNA Library Preparation: Open Blosystems

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AlaGly 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii, Neopterygii, Teleostei, Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThr 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           565 GGGCACAGTGGGGTGACCCATCACCAGAGTCCATCACGATACCAGTGGTACGACC 509
/clone lib="NCI CGAP_ZKidl"
/nocle="Organ: Kidney, Vector: pCMV-SPORT6.1; Site_1:
/nocle="Organ: Kidney, Vector: pCMV-SPORT6.1; Site_1:
COSWY; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.8 kb. Constructed by J
Wang (Research Genetics, Invitrogen Corp) from tissue
donated by L. Zon (Harvard University). Note: this is
NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 ThralaPheleuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 ValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 GlnIleArgSerGlyGlyGerProThrValHisIle-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 GlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIle-
                                                                                                                                                                                                                                                                                                            907
117
117
117
117
```

us-09-684-215b-23.rst

```
/tissue_type="whole body"
/lab_host="whole body"
/lab_host="DH10B"
/clone_lib="WH ZGC_"
/note="Vector: pExpress!; Site_1: Not!; Site_2: EcoRV;
/note="Vector: pExpress!; Site_1: Not!; Site_2: EcoRV;
/note="Vector: pExpress!; Site_1: Not!; Site_2: EcoRV;
/note="Vector: pExpress!; Site_1: Not! individual
from the Tuebhingen strain. ist strand oDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments and
normalized. A non-normalized version of this library is
also available (NIH ZGC 10). Library was constructed by
Open Biosystems (Huntsville, AL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      658 -----TICCCTCTCAGCIGIGGIGGIGAAGCIGIAGCTCTCTCTCGGCAGAICTICAI 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------LeuAsnGlyHisHisProGlyAspValileSerValThrTrpGlnThrLyB 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          706 AAAGTCAAGGGCCACATAGCAGACTTCTCCTTGATGTCACGGACAAT------ 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            766 AGCAGTICGIAGCICTICICCAGGAGGÁGGÁGGÁGGÁGCAGCGGIGCCCÁTCICCIGCIC 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 GlnGlyGlyGlnGlyPheAlaIleProlleGlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 ------GlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGly 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 AspValileThrAlaValAspGlyAlaProileAsnSerAlaThrAlaMetAlaAspAla 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 Arg----- 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 AlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGly 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerGlyGlyThrArg-----ThrGlyAsnVal 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 AGTGGTACGACCAGAGGCATACAGGGACAGCACGCACGCTGGATGGCAACGTA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
             column: 09
                                                                                          /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:6996778"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-684-215B-23 (1-128) x CF265501 (1-913)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: April 30, 2004, 04:41:02 Job time : 2510.02 secs
Plate: LLAM14682 row: j col.
High quality sequence stop: 6
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.6
93.50
37.96%
27.01%
14.36%
                                                                             .. .913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \dot{\delta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \stackrel{>}{\circ}
```

```
3 06:36:18 2004
```

us-09-684-215D-23.rnı

		Ç	,	6	0	-	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	
	GenCore version 5,1,6	14	646	99.2	1872	1, 4, D D	US-09-038-17	
	Copyright (c) 1993 - 2004 Compugen Ltd.	15	646	99.2	1872		US-09-072-967-17	
		16	608 608	93.4 93.4	675 675	4. 4. D D	US-09-636-215-822 US-09-685-166A-822	
OM protein - nu	OM protein - nucleic search, using frame plus p2n model	18	608	93.4	822	4	US-09-736-457-1862	
	1	19	809	93.4	900	4	US-09-643-597-353	
Run on:	April 29, 2004, 22:28:57; Search time 65.5311 Seconds	20	809	93.4	900	4 U	US-09-606-421B-353	
	(without alignments)	21	608	93.4	912		US-09-636-215-834	
	1083.969 Million cell updates/sec	22	608	93.4	915		US-09-685-166A-834	
	(117 70 00 01	200	800	7 7	0.42	* *	110 - 00 - 730 - 40 / - 100 I	
11016:	57-95-77-77-77-77-77-77-77-77-77-77-77-77-77	7 C	0 0	4.00	101	,,	100 - 100 - 100 - 100 THE	
Semience:	1 TAASDNFOLSOGGGRATTI SVINOTKSGGTRIGNVILAE 128	2 7	909	2. 6. 4. 4.	1203	. 4	US-09-636-215-331 US-09-636-215-851	
		27	608	93.4	1203	4. D	US-09-685-166A-851	
Scoring table:	BLOSUM62	28	608	93.4	1464	4	US-09-620-412C-348	
ı		29	608	93.4	1464	4 U	US-09-598-419-348	
		30	608	93.4	1557	₽	US-09-620-412C-332	
	Fgapop 6.0 , Fgapext 7.0	31	608	93.4	1557	4 D	US-09-598-419-332	
		32	608	93.4	1578	4	US-09-556-877-188	
		33	609	93.4	1578	4	US-09-620-412C-188	
Searched:	682709 segs, 277475446 residues	34	609	93.4	1578	4	US-09-598-419-188	
		35	609	93.4	1752	4.	US-09-620-412C-352	
Total number of	Total number of hits satisfying chosen parameters: 1365418	36	609	93.4	1752	4	US-09-598-419-352	
		37	608	93.4	1758	4	US-09-620-412C-336	
Minimum DB seq	length: 0	38	608	93.4	1758	4	US-09-598-419-336	
Maximum DB seq	Maximum DB seq length: 2000000000	39	608	93.4	1860	4	US-09-620-412C-308	
		40	608	93.4	1860	44	US-09-598-419-308	
Post-processing	: Minimum Match 0%	41	608	93.4	1896	4	US-09-620-412C-324	
	Maximum Match 100%	4.2	608	93.4	1896	4	US-09-598-419-324	
	Listing first 45 summaries	43	608	93.4	1941	4	US-09-620-412C-316	
		44	809	93.4	1941	4	US-09-598-419-316	
Command line parameters:	rameters:	45	809	93.4	1965	4	US-09-620-412C-340	

Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 182, App Sequence 182, App Sequence 183, App Sequence 181, App Sequence 188, App

```
GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Bllon, Davin C.

APPLICANT: Dillon, Mark

APPLICANT: Campos-Neto, Antonio

TITLE OF INVENTION: and Their Uses

FILE REFERENCE: 014058-00920US

CURRENT PAPLICATION NUMBER: US 08/09/287, 849

PRIOR FILING DATE: 1999-04-07

PRIOR PELING DATE: 1999-02-18

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR PRIOR APPLICATION NUMBER: US 09/056,556

PRIOR PRIOR APPLICATION NUMBER: US 09/223,040

PRIOR APPLICATION NUMBER: US 09/223,040

PRIOR PRIOR APPLICATION NUMBER: US 09/223,040

PRIOR FILING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 27

LIBRICH: 702

LIBRICANT: 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:bl-fusion
OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading
OTHER INFORMATION: frame 1
ALIGNMENTS
                                                                                                                                    Sequence 27, Application US/09287849; Patent No. 6627198; GENERAL INFORMATION:
                                                                        RESULT 1
US-09-287-849-27
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUG_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUG_COMB.seq:*

Database :

Sequence 27, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 17, Appli

US-09-287-849-27 US-09-223-040-1 US-09-2103-840A-1 3 US-09-103-840A-1 US-08-818-112-4 US-08-818-111-4 US-09-056-556-4 US-09-072-596-4 US-09-072-596-4 US-09-018-111-17 US-09-018-111-17 US-09-018-111-17

100.0 2287 4 UU 100.0 2287 4 UU 100.0 4403765 3 UU 100.0 4411529 3 1 UU 100.0 4411529 3 UU 100.0 4411529 3 UU 100.0 4411529 3 UU 100.0 4411529 3 UU 100.0 4417 4 UU 100.0 4417

2642676992

Description

Length DB

Query Match

Score

Result

```
205 GICCAACGCGIGGICGGGGGCGCTCCGGCGAAGICTCGGCCAICTCCACCGGCGACGTG 264
                                                                                                                                                                                                                                                                                                                                                                                                      81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                  265 ATCACCGGGTCGACGGCGCTCCGATCAACTCGGCCACGCGATGGCGGGACGCGTTAAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGGGGGCGCGCGT 384
                                                                                                                                                                                                                                                                                                                                144
                                                                                                                                                                                                                                                                                                                41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAshgArg 60
                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                             21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                   61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlylleSerThrGlyAspVal
DOCATION: (1) .. (693)
OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
OTHER INFORMATION: reading frame 1
NAME/KEY: CDS
LOCATION: 12) .. (700)
CHER INFORMATION: reading frame 2
NAME/KEY: CDS
CHER INFORMATION: reading frame 3
CHER INFORMATION: reading frame 3
US-09-287-849-27
                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                        US-09-684-215B-23 (1-128) x US-09-287-849-27 (1-702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385 ACAGGAACGTGACATTGGCCGAG 408
                                                                                                                              4.03e-64
651.00
100.00%
100.00%
                                                                                                                   Alignment Scores:
9red. No.:
Score:
Percent Similarity: 1
Pest Local Similarity: 1
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-09-223-040-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \stackrel{>}{\circ}
                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ଚ
                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                            જે
                                                                                                                                                                                                                                                                                                                                                                                                  8
```

```
US-US-ZB/-849-1

Sequence 1, Application US/09287849

Patent No. 6627198

GENERAL INFORMATION:
APPLICANT: Read, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Sheiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Contact Corporation
APPLICANT: DATE: 1999-04-07
APPLICANT: DATE: 1997-03-13
APPLICANT: PRICE 1997-03-13
APPLICANT: PRICE 1997-10-01
APPLICANT: PRICE 1998-02-18
APPLICANT: PRICE 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 ileThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                182
                                                                                                                                                                                                                                                                                                                  242
                                                                                                                                                                                                                                                                                                                                                                      243 GICCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 302
                                                                                                                                                                               63 ACGGCCGCCCCATAACTTCCAGCTGCCCAGGGGGGCAGGGATTCGCCATTCCGATC 122
                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                  60
                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                  41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                      61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                    1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlalleProlle
                                                                                                                                                                                                                    21 GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
   228
0000
0000
   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                   US-09-684-215B-23 (1-128) x US-09-223-040-1 (1-2287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ThrGlyAsnValThrLeuAlaGlu 128
Score:
Score:
Fercent Similarity:
Best Local Similarity:
Cuery Match:
DB:
                                                                                                                                                      ò
                                                                                                                                                                             8 8 8
                                                                                                                                                                                                                                                                             8 8 8
                                                                                                                                                                                                                                                                                                                                                                              원 수 명
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
```

or

U

Alignment Scores:

ö ö

U

NAME/KEY: modified_base

LOCATION: (10)

NAME/KEY: modified_base

LOCATION: (33)

OTHER INFORMATION: n = g, a, c

NAME/KEY: CDS

LOCATION: (42)...(2231)

NAME/KEY: modified_base

LOCATION: (42)...(2231)

NAME/KEY: modified_base

LOCATION: (2270)

OTHER INPORMATION: n = g, a, c

US-09-223-040-1

O

```
101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 erccaacecereerceegaececreceeceecaaercreecarcreecaeceaecere 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 ACGGCCGCCCGATAAATTCCAGCTGTCCCAGGGTGGGGAGGAATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle
                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39 OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39 OTHER INFORMATION: 100 Included base Information: 100 Information: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2287
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-684-215B-23 (1-128) x US-09-287-849-1 (1-2287)
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR PELLOATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2287
TYPE DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 ACAGGGAACGTGACATTGGCCGAG 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , LOCATION: (2270)
, OTHER INFORMATION: n = g, a, c (
US-09-287-849-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.92e-63
651.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 2436-24007-00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765

positions throughout the g

various ;

TYPE: DNA ORGANISM: Mycobacterium tuberculosis

FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at
OTHER INFORMATION: represent a,

Length:
Matches:
Conservative:
Mismatches:

4.178-59 651.00 100.00% 100.00%

Alignment Scores: Pred. No.:

; OTHER INFORM US-09-103-840A-2

```
81 ileThralaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09103840A

Sequence 1, Application US/09103840A

Setent No. 6224438

GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REPRESENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT PILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SEQ ID NO(1)
                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                40
                                                                                                                                                                                                                                             9
                                                                                                                 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                              21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                           ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                            41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                       101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                   US-09-684-215B-23 (1-128) x US-09-103-840A-2 (1-4403765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152344 ACAGGGAACGTGACATTGGCCGAG 152367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ThrGlyAsnValThrLeuAlaGlu 128
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઢ
                                                                                                                   ò
                                                                                                                                                원
                                                                                                                                                                                ઠે
                                                                                                                                                                                                             а
                                                                                                                                                                                                                                                 ઠ
```

GENERAL INFORMATION:
APPLICANT: FLEISCHWAN, ROBERT D.
APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.

```
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: MAKT, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-112-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152115 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCACGCGT 152174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151995 GICCAACGCGIGGICGGGAACGCTCCGGCGAAGTCTCGGCATCTCCACCACGAACGTG 152054
                                                                                                                                                                                                                                                                                                                                     151874
                                                                                                                                                                                                                                                                                                                                                                                                            151935 Arceseccificeccificercideserreseristresecateaacaacaaceaaceaaceaacaacaacaacaacaacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 ileThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                          40
                                                                                                                                                                                                                                                                                                                     151815 ACGCCCGCTCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGATCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                          GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08818112;
Sequence 4, Application US/08818112;
Patent No. 6290969;
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Repair A.W.
APPLICANT: Campos-Neto, Antonio APPLICANT: Campos-Neto, Antonio APPLICANT: Twardzik, Daniel R.
ANDRESSES: SEDDANSS:
ADDRESSES: SEDD and BERRY LIP
                                                                                                                              4411529
128
                                                                                                                                                                                                                                                               US-09-684-215B-23 (1-128) x US-09-103-840A-1 (1-4411529)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 98104-7092
COMPUTER RADABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152175 ACAGGGAACGTGACATTGGCCGAG 152198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrGlyAsnValThrLeuAlaGlu 128
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                              4.186-59
651.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washing
                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-818-112-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

13-MAR-1997

```
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 dedelarcarcecedade de contra de como de como de contra de cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                                                                                                                                                                                                    70
                                                                                                                                                                                                                                                                                                                                                                       21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 Arceeeccraceccrrccrceecrreerrerrerrereacacacaacaaceaceecececa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                                                                                                          1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProlle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOR DIAGNOSIS OF
                                 447
1127
1
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence A. Application US/08818111
| Patent No. 6338852 | GENERAL INFORMATION: APPLICANT: Real Stein A. W. APPLICANT: Resiry, Yasir A. W. APPLICANT: Campos-Neto, Antonia APPLICANT: Houghton, Raymond APPLICANT: Vedvick, Thomas S. APPLICANT: Tractaik, Daniel R. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR NUMBER OF SEQUENCES: 148 | CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                        US-09-684-215B-23 (1-128) x US-08-818-112-4 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 ACAGGGAACGTGACATTGGCCGAG 394
                                                                     646.00
99.22%
99.22%
99.23%
                                                                     Percent Similarity: 5
Best Local Similarity: 9
Query Match: 9
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SEE
STREET: 6300 C
CITY: Seattle
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            경. 점
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ठे
                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

```
TREATM
```

PREVENTION AND

THE

```
COMPOUNDS AND METHODS FOR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
Percent Similarity:
9
Best Local Similarity:
9
Query Match:
4
   INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-056-556-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-09-072-596-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 GTCCAACGCCTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCCACCGGCGACGTG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAGGCAACGGCGCACGA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 ACGGCCGCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValGinArgValValOlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAla1leProIle
                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-23 (1-128) x US-08-818-111-4 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 ACAGGGAACGTGACATTGGCCGAG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09056556 Patent No. 6350456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Reed, Seeven G.
APPLICANT: Skeiky, Yesir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.06e-64
646.00
99.22*
99.23*
 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-818-111-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-056-556-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
```

g ò g 8

```
130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 Arceseccracescricercesecries and a second caracterates and consequences of the contract of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 ileThralaValAspGlyAlaProileAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ACGGCGCGTCCGATAACTTCCAGCTGTCCCAGGGGGGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlydlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 IleGlyProThrAlaPheLeuGlyLeuGlyValValValAspAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGGCACGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
TITLE OF INVENTION:

NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STARE: Washington
COUNTRY: Washington
COUNTRY: RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRANT APPLICATION NUMBER: US/09/056,556
FLIING DATE: O7-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MARK, DAYLG J.
REGISTRATION NUMBER: 31,392
REFERENCE CLOS/ 662-6031
TELEFHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STARNEDDRESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447
1127
0
1
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-23 (1-128) x US-09-056-556-4 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 ACAGGGAACGTGACATTGGCCGAG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      646.00
99.22%
99.22%
99.23%
```

250

쉽 à g

D_D ò

 δ

8 8 8

80

09.

40

Page

```
121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                        371 ACAGGGAACGTGACATTGGCCGAG 394
                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09072967
Patent No. 6592877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score: 646.00
Percent Similarity: 99.22*
Per Local Similarity: 99.22*
Query Match: 99.23*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 447 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic ac:
STRANDEDNESS: sii
TOPOLOGY: linear
US-09-072-967-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                   RESULT 10
US-09-072-967-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ਨੇ
                                                             ઠે
                                                                                                                    ď
                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 ATCGGGCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCAACGGCGCACGA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ACGGCCCCCGTCCCGATAACTTCCCAGCTGTCCCAGGGTGGGCAGGGATTCCCCATCCCATC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GlyGlnAlaMetAlaileAlaGlyGlnileArgSerGlyGlyGerProThrValHis 40
                                                                                     APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES. 350
CORRESPONDENCES. 350
CORRESPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447
127
0
1
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Washington
COUNTRY: USA
ZIP: 98104-705
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-23 (1-128) x US-09-072-596-4 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-690
TELEPAX: (206) 682-691
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
4, Application US/09072596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          999.222#
999.222#
99.222#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 C
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-072-596-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                     101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                     311 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGGCGCGCGT 370
251 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ThralaalaseraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaileProile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 ACGCCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHODS FOR IMMUNOTHERAPY OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                            GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Reed, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Hendrickson, Ronald C.
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNC
TILLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEDS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
CITY: Seattle
STREET: MEDIUM TYPE: Floppy disk
COMPUTER READALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER SEADALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER SEATINON DATA: US/09/072;967
FILING DATE: 05-WAY-1998
CLASSIFICATION NUMBER: US/09/072;967
FILING DATE: NUMBER: US/09/072;967
ATTONEY AND NUMBER: US/09/072;967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-215B-23 (1-128) x US-09-072-967-4 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
RECISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
```

```
셤
                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                   ठे
                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                           81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                               131 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTCGACAACGGCAACGGCGCACGA 190
                                                                                                                                                                                       80
                                                                                                                                                                                    61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                   41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-00-818-112-17
US-00-818-112-17
Sequence 17, Application US/08818112
Septicant Skeiky, Yasir A.W.
APPLICANT Skeiky, Yasir A.W.
APPLICANT Campos-Neto, Artonic
APPLICANT USAGEON ARTONIC
APPLICANT TWARATION. AND DAGNOS FOR INMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
COMPUTER REQUINCES: 153
KNUMBER OF SEQUENCES: 153
KNUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 ACAGGGAACGTGACATTGGCCGAG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.34e-63
646.00
99.22%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-818-112-17
                                 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                         ठ
                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                  ď
```

```
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              998 AICACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGAGGCGCGTTAAC 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                   817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   878 Arceegecracceccriccroegerreegrericateacaacaacegeaaceacaacea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   938 grechaegegregregadegerecegegegaagregegaagreregecarerecegegege 997
                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                       1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                       758 ACGGCCGCGTCCGATAACTTCCAGCTGCTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                    21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                  818 GGGCAGGCGATGGCGATCGCGGGCCAATCCGATCGGGTGGGGGGTCACCCCACCGTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 IleGlyProThrAlaPheLeuGlyLeuGlyValValNalAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-08-818-111-17
US-08-818-111-17
Sequence 17, Application US/08818111
Patent No. 6138852
Fatent No. 61388852
Fatent No. 6138852
Fatent No. 6138853
Fatent 
                                                                                                                                                            US-09-684-215B-23 (1-128) x US-08-818-112-17 (1-1872)
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1118 Acadedaacerdacarredeceae 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ThrGlyAsnValThrLeuAlaGlu 128
    99.22%
    Best Local Similarity:
Query Match:
DB:
```

```
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1117
                                                                                                                                                                                                                                                                                                                                                                                             817
                                                                                                                                                                                                                                                                                                                                                                                                                                                            877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                938 GICCAACGCGTGGTCGGAAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 997
                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                              101 GlyHisHisProGlyAspVallleSerValThrITpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                                                                                                                                                           758 Aceeccececcearaacriccaecrereccaesesesesesesarreseare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                               1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlalleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-072-596-17

Sequence 17, Application US/09072596

Sequence 17, Application US/09072596

Patent No. 6458366

GENERAL INFORMATION:
APPLICANT: Reed's Steven G.
APPLICANT: Campose-Neto, Antonia APPLICANT: Campose-Neto, Antonia APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson Compounds AND METHODS FOR DIAGNOSIS OF THE OF TRYBERT: 6300 Columbia Center, 701 Fifth Avenue CITY: Seatle STREET: Mashington COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                             1872
127
10
0
0
                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                US-09-684-215B-23 (1-128) x US-09-056-556-17 (1-1872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ThrGlyAsnValThrLeuAlaGlu 128
REFERENCE/DOCKET NUMBER: 210
TELEPOMMINICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INPORMATION FOR END ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                   5.34e-63
646.00
99.228
99.228
                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                 US-09-056-556-17
                                                                                                                                                                                                                   No.:
                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ठ व ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TREAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          938 GTCCAACGCGTGGTCGGAAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTG 997
                                                                                                                                                                                                                                                                                                  817
                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlylleSerThrGlyAspVal 80
                                                                                                                                                                                                                                                                    50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-05-55-56-17

Sequence 17, Application US/09056556

Patent No. 6350456

GENERAL INPORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Davin C.
TILLE O'NERESPONDENCES: 241
CORRESPONDENCES: 241
CORRESPONDENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seatile
STATE: Washington
COUNTY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY JAVIG J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                758 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                      878 ATCGGGCCTACCGCCTTCTCGGGCTTGGGTGTTGTCGACAACAACAACGGCACGA
                                                                                                                                                                                                                                                                    1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                  41 IleGlyProThrAlaPheLeuGlyVeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                    US-09-684-215B-23 (1-128) x US-08-818-111-17 (1-1872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1118 ACAGGGAACGTGACATTGGCCGAG 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                5.34e-63
646.00
99.228
99.228
     LENGTH: 1872 base pairs
                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                     Percent Similarity:
Best Local Similarity: 9
Query Match:
DB:
                                                    ,
TOPOLOGY:
US-08-818-111-17
                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
```

g ò 셤

g ò

g ò

8

g ઠે g

ò

```
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SUSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAM:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
NAMME: MAKI, DAVId J.
ATTORNEY/AGENT INFORMATION:
NAMME: MAKI, DAVId J.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (206) 682-6031
INFORMATION FOR EQL ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
INFORMATION FOR EQL ID NO: 17:
SEQUENCE CHARACTERISTICS:
CHARACTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.34e-63
646.00
99.22%
99.22%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-072-596-17
```

US-09-684-215B-23 (1-128) x US-09-072-596-17 (1-1872)

Gaps:

```
998 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGTTAAC 1057
                                                                                                                                                                                                                                                                                                          101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                        81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaWetAlaAspAlaLeuAsn 100
                            817
                                                                                  877
                                                                                                                                        937
                                                                                                                                                                                938 GTCCAACGCGTGGTGGGAAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 997
                                                       40
                                                                                                              9
                                                                                                                                                                    80
              21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                         818 GGGCAGGCGATGGCGATCGCGGGCCAAATCCGATCGGGTGGGGGGTCACCCCACCGTTCAT
                                                                                                                             41 ileGlyProThrAlaPheLeuGlyVeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                         1118 ACAGGGAACGTGACATTGGCCGAG 1141
                                                                                                                                                                                                                                                                                                                                        ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                        121
                      셤
                                                                          ద
                                                                                                           ò
                                                                                                                                  g
                                                                                                                                                           8 8 8
                                                                                                                                                                                                                                             쉱
                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                       8
ò
                                                    ò
```

```
Sequence 17, Application US/09072967; Patent No. 6592877; GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio, APPLICANT: Houghton, Raymond; APPLICANT: Vedvick, Thomas S.
RESULT 15
US-09-072-967-17
```

```
817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodge, Michael J.
APPLICANT: Lodge, Michael J.
APPLICANT: Lodge, Michael J.
APPLICANT: CANDON Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: Washington
COUNTRY: USA
CONTRY: USA
ZIP: 98104-7092
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BAPENSIE FORM:
MEDIUM TYPE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/072,967
FILING DATE: OS-MAY-1998
CLASSIFCATION NUMBER: US/09/072,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-684-215B-23 (1-128) x US-09-072-967-17 (1-1872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
NAME: Maki, David J.
NAME: Maki, David J.
NAME: Maki, David J.
REGISTATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 210121.411C9
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-631
INFORMATION FOR ENQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TEMBETH: 1872 base pairs
TEMBETH: 1872 base pairs
TEMPETH: 1872 base pairs
TEMPETH: 1872 base pairs
TOPOLOGY: 11near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
```

40 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 8 g 원

```
Mon May 3 06:36:18 2004
```

1118 ACAGGGAACGTGACATTGGCCGAG 1141

113-02-02T7-884-60-80-

370 ACAGGGAACGTGACATTGGCCGAG 393

```
82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAG------CTTCCCACCGTTCAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleThralaValaspGlyalaProlleAsnSeralaThralaMetalaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 IleGlyProThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
US O9-638-215-82

Sequence 822, Application US/09636215

Patent No. 6620922

GENERAL INFORMATION:

APPLICANT:

APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               675
1122
11
14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-23 (1-128) x US-09-636-215-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.486-59
608.00
96.09%
95.31%
93.39%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-09-636-215-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

ThrGlyAsnValThrLeuAlaGlu 128

310

121

101

ઠે

```
81 IleThralayalaspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 IleglyProThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                               GENERAL INVEXMATION:
GENERAL INVEXMATION:
APPLICANT:
AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-23 (1-128) x US-09-685-166A-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrGlyAsnValThrLeuAlaGlu 128
RESULT 17
US-09-685-166A-822
Sequence 822, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.48e-59
608.00
96.09%
95.31%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CRGANISM: Homo sapiens
US-09-685-166A-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

118-03-684-713D-73.ru

370 ACAGGGAACGTGACATTGGCCGAG 393

d

THE THERAPY

APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Mang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Woneill, Paricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE FILE REPERBORE: 210121.455011
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: PastSEQ for Windows Version 3.0
EBRICTH: 900

```
21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR THE THERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215B-23 (1-128) x US-09-736-457-1862 (1-822)
                                                                                                             GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Carter, Gary
APPLICANT: Varier, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Fan, Ligun
APPLICANT: Fan, Ligun
APPLICANT: Fan, Ligun
APPLICANT: Fan, Ligun
APPLICANT: Pan, Ligun
APPLICANT
APPLIC
                             Sequence 1862, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.22e-59
608.00
96.09%
95.31%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
US-09-736-457-1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-09-736-457-1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

```
RESULT 20
US-09-606-421B-353
                                                                                                                          ઠે
                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                     82 GGGCAGGCGAIGGCGAICGCGGGCCAGAICAAG------CIICCCACCGIICAI 129
                                                                                                                                                                                                               130 ATCGGGCCTACCGCCTTCCTCGCTTGGGTGTTGTCGACAACAACAACGGCACGCGCACGA 189
                                                                                                                                                                                                                                                                                                                      81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                250 ATCACCGCGGTCCACGCGCTCCCGATCACTCGGCCACCGCGATGGCGGACGCGCTTAAC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 GGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 369
                                                                                                                                                                                    IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                                              61 ValGlnArgvalValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                              1 ThralaalaSeraspasnPheGinLeuSerGinGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 ACAGGGAACGIGACATTGGCCGAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 19
US-09-643-597-353
VS-09-ence 353, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
```

g

g 8

```
82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAG-----CTTCCCACCGTTCAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 GICCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGAACGTG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 ileThralaValAspGlyAlaProileAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 369
                                                                                                                                                                                                                                                                                                                                              21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                          41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspVal
                                                                                                                                                                                                                                                                                        22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                US-09-684-215B-23 (1-128) x US-09-643-597-353 (1-900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 353, Application US/09606421B
Patent No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ThrelyAsnValThrLeuAlaglu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 acadedacerdacarrecedae 393
                                                                                      3.638-59
608.00
96.09%
95.31%
TYPE: DNA
CRGANISM: Homo sapiens
US-09-643-597-353
                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                               업
                                                                                                                                                                                                                                                                       ਨੇ
                                                                                                                                                                                                                                                                                                                                                ઠે
```

```
IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 Grecalcecerecrececacecreceseses 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 ileGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ACGGCCCGCGTCCCGATAACTTCCCAGCTGTCCCAGGGTGGCCAGGGATTCGCCATTCCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
APPLICANT: Wang, Aijun APPLICANT: Wang, Aijun APPLICANT: Skeiky Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE STORTICANION NUMBER: US/09/606,421B
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FSSESSQ for Windows Version 3.0
SEQ ID NO 353
LENGTH: 900
                                                                                                                                                                                                                                                                                           0011141
002
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-215B-23 (1-128) x US-09-606-421B-353 (1-900)
                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 834, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: V. Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Johnif Er L.
APPLICANT: Mitcham, Connifer L.
APPLICANT: Mitcham, Connifer L.
APPLICANT: Mitcham, Nobert A.
APPLICANT: Fanger, Raine, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Darrick
APPLICANT: Vanage R.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 ACAGGAACGTGACATTGGCCGAG 393
                                                                                                                                                                                                                                                                                             3.63e-59
608.00
96.09%
95.31%
                                                                                                                                                                                                         TYPE: DNA
CRGANISM: Homo sapiens
US-09-606-421B-353
                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 21
US-09-636-215-834
                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                    Query Match:
DB:
                                                                                                                                                                                                                                                                                                  ..
02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      상 점
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
```

```
369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 IleThralaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 ATCACCGGGTCGACGGCGCTCCGATCAACTCGGCCACGCGGATGGCGGGATGAAC309
                                                                                                                                                                                                                                                                                                                                                         82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAG------CTTCCCACGTTCAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                             130 Arcedectacceccrrcraegringererereacaacaacaacaacaaceacaacea 189
                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ValGinArgValValGiySerAlaProAlaAlaSerleuGiyIleSerThrGiyAspVal 80
                                                                                                                                                                                                                                                                               22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCATTCCGATC
                                                                                                                                                                                                                                                                                                                                   40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 gegearcarecegagasearcarecegaaceregeaaaceaagregegegeeer
                                                                                                                                                                                                                                                                                                                                                                                                             41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                          1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyBheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                   21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                        US-09-684-215B-23 (1-128) x US-09-636-215-834 (1-915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-685-166A-834

Sequence 834, Application US/09685166A

Patter No. 6630305

GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Handerson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Marc M.
APPLICANT: Ranger, Marc M.
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Bay, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Li, Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 acadedacerdacarrecedad 393
                                                                              3.71e-59
608.00
96.09$
95.31$
TYPE: DNA
COGANISM: Homo sapiens
US-09-636-215-834
                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                       \dot{\delta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
```

THE THERAPY AND

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER;
TILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 834
LENGTH: 915

Wang, Aijun

```
82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAG------CTTCCCACCGTTCAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCACGAGGAGCTG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 GGGCATCATCCCGGTGATCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 Arcedeccracecerrececraeserraserereserareseraseaseaseseseses 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 Arcaccaccarcaaccaccarccarcaacrosscaccaccaccacacacaccaccaccacriaac 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 Acescececercearraacriceaecrereceaeseresecaesearresecarreceare 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42.72.1
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT APPLICATION NUMBER: US/09/685,166A
SOFTWARE: Past SEQ ID NOS: 898
SOFTWARE: Past SEQ for Windows Version 3.0
EBNOTH: 915
TYPE. P.C.
TYPE. P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-736-457-1861

Sequence 1861, Application US/09736457

Patent No. 6509446

APPLICANT: Wang, Tongtong

APPLICANT: Lodes, Michael A.

APPLICANT: Lodes, Michael A.

APPLICANT: Panger, Gary

APPLICANT: Panger, Gary

APPLICANT: Patenter, Darrick

APPLICANT: Retter, Marc

APPLICANT: Retter, Marc

APPLICANT: Pannion, Jane

APPLICANT: Fan, Liqun

APPLICANT: Pan, Liqun

TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.478C15

CURRENT APPLICATION NUMBER: US/09/736,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-684-215B-23 (1-128) x US-09-685-166A-834 (1-915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 ACAGGGAACGTGACATTGGCCGAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.71e-59
608.00
96.09%
95.31%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo sapiens
US-09-685-166A-834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAG------CTTCCCACGTTCAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 666CATCATCCCGGTGACGTCATCTCCGTGACCTGGCAAACCAAGTCGGCCGCCACGCGT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ACGGCCCCGTCCCGATAACTTCCAGCTGTCCCAGGTGGGGTGGGGATTCGCCATTCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 GICCAACGCGIGGICGGCGCGCCCGCCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ValGlnArgValValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                          1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chattanya S.
APPLICANT: Bangur, Chattanya S.
APPLICANT: Hanger, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Parricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Mindows Version 3.0
SEQ ID NO 351
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-23 (1-128) x US-09-736-457-1861 (1-945)
                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
Indels:
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SEQ YARRE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1861
; LENGTH: 945
; TYRE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 ACAGGGAACGIGACATTGGCCGAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 24
US-09-643-597-351
Sequence 351, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
                                                                                                                                                                                                                  Score: 3.87e-59
Score: 608.00
Percent Similarity: 96.09#
Query Match: 95.31#
DB:
                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             දු දු
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

126

174 40

234

9

294

80

8

à

```
67 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATCCGATC
                                                                                                                                                           21 GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGerProThrValHis
                                                                                                                                                                                41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                      ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE THERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NESULY 26

US-09-636-215-851

Sequence 851, Application US/09636215

Sequence 851, Application US/09636215

Sequence 851, Application US/09636215

Sequence 851, Application US/09636215

Septeman Incompanies Inc
                                                  US-09-684-215B-23 (1-128) x US-09-606-421B-351 (1-1012)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 ACAGGGAACGTGACATTGGCCGAG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.32e-59
608.00
96.09%
95.31%
93.39%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                        8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                      Д
                                                                                                                                                                                                                                                                                                  ò
                                                                                           ò
                                                                                                                                                       ઠ
                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                    41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1012
122
1
                                                                         1012
122
14
14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 25
US-09-606-421B-351
Sequence 351, Application US/09606421B
Patent No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fanger, Caitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Aljun
APPLICANT: Skeiky, Yasir A.W.
ITILE OF INVENTION: COMPOSITIONS OF LUNG CANCER
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                   US-09-684-215B-23 (1-128) x US-09-643-597-351 (1-1012)
                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.24e-59
608.00
96.09%
95.31%
                                                                       4.246-59
608.00
96.09%
95.31%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CRGANISM: Homo sapiens
US-09-606-421B-351
       ; ORGANISM: Homo sapiens
US-09-643-597-351
                                                    Alignment Scores:
Pred. No.:
Score:
Fercent Similarity:
Best Local Similarity:
Ouery Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                       8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                    경염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \dot{\delta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

4,	US-09-684-215B-23 (1-128) x US-09	AlaileProile 20		A1	IGTYSerAlaProAlaAlaSerLeuGly11eSerThrGlyAspVal 80 QY	pglyalaProlleAsnSeralaThrAlaMetAlaAspalaLeuAsn 100 Qy 81 IleThrAlaValAspGlyAlaProlleAs		Qy	RESULT 28 Sequence 348, Application US/09620412C Squence 1	
٦,	3)	yGlnGlyPhe GCAGGGATTO	yGlyGlyser	pasnasngly. caacaacggc	uGlylleSer CGGCATCTCC	ralaMetAla GCGATGGCG	nThrLysSer AACCAAGTCG		THE THERAPY 1203	
	-851 (1-1203	spasnPheGlnLeuSerGlnGlyGlyGlyGlyPhealaileProil 	: : : : : : : : : ATCAAG	GlyvalvalAs GGTGTTGTCGA	AlaAlaSerLe GCGGCAAGTCT	AsnSeralaTh AACTCGGCCAC	1yHisHisProGlyAspVallleSerValThrTrpGlnThrLysS 	o m	S FOR CANCER	
	9-636-215-851	pAsnPheGlnLeus 	allealaGlyGlnIleArg ::: :GATCGCGGGCCAGATCAAG	LeuglyLeu(CTCGGCTTGC	SerAlaPro/ AGCGCTCCGC	Alabrolle GCTCCGATC	valileser Grcarcrcc	Alaglu 12 cccas 39	. AM P P) 19/6 rrsiú	
	×	aSerAspAsn 3TCCGATAAC		orhralaphe AccGcctrc		avalAspGlyAlaP GGTCGACGGCGCTC	BProGlyAsp rcccggrgAC	# <u>-</u> #	ation gchun Joavin Joavin Goby Goby Goby Goby Joan	
	3-23 (1-128)	ThrAlaAlaSerAs	GlyGlnalametal GGGCAGGCGATGGC	IleGlyProThrA 	ValGlnArgValVa 	ileThral	დ—ტ	ThrGlyAsnValTh	A 851 A Application U 663305 DRWATION: Xu, Jiangchun Dillon, Davin, Mitcham, Jenni Harlorer, Sus Jiang, Yuqui Handerson, Rob Handerson, Rob Handerson, Rob Handerson, Rob Jenni Hanger, Gary R Retter, Marc W Rence: Li, Samuel Nordyick, Thoma Cate of Marc W Reserved Li, Samuel Repler, Willia Rence: Li, Samuel Reserved Reserve	
	US-09-684-215B-23	22 1	21 8 8 2	41	190	81	101	121	VG-09-665-1654-851 VG-09-665-1654-851 Sequence 851 Application Sequence 851 Application GENERAL INFORMATION: APPLICANT: Wilcham, John APPLICANT: Harlocker, SI APPLICANT: Harderson, RA APPLICANT: Handerson, RA APPLICANT: Fanger, Gary APPLICANT: Fanger, Gary APPLICANT: Fanger, Gary APPLICANT: Fanger, Carig H APPLICANT: Griff, Thon APPLICANT: Griff, Thon APPLICANT: Bay, Craig H APPLICANT: Bay, Craig H APPLICANT: Griff, Thon APPLICANT: Griff, Will: APPLICANT: Hepler, Wil	
DB:	US-0	В Q	ζ O O O	Qy Dp	97 10 10 10 10 10 10 10 10 10 10 10 10 10	දු දු	දු පු	දු දු	RESULT US-09-09-09-09-09-09-09-09-09-09-09-09-09-	

```
AsnSeralaThralaMetAlaAspalaLeuAsn 100
                                                                                                                                                                                                                                    ValThrtpGlnThrlysSerGlyGlyThrarg 120
                                                                                                                                                          AlaalaSerLeuGly1leSerThrGlyAspVal 80
                                                                                 GlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IleargserGlyGlyGlySerProThrvalHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glyvalvalaspasnasnglyasnglyalaarg 60
                                             SerGlnGlyGlyGlnGlyPheAlaileProile 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerginglyglyglnglyPheAlaileProile 20
                                                                                                                                                                                                                                                                                                                                                                        ETHODS FOR TREATMENT AND MYDIAL INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 1464
fatches: 122
Conservative: 1
fismatches: 4
indels: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-348 (1-1464)
                            A-851 (1-1203)
dels:
ps:
```

100 129 189 GICCAACGCGIGGICGGGGGCTCCGGGGGAAGICTCCGGCATCTCCACGGCGACGTG 249 Arcaccecedescedescentesarcaacrescentescearescentescentescentase GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120 369 100 309 9 80 101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40 190 erccaacecerecreeceacecrecesesearererecatererecatereseares 20 81 80 82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAGG------CTTCCCACCGTTCAT 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn dedeateatecedergaegreateregergaectegeraaceaagregegegegeger 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn ValGinargValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal Sequence 348, Application US/09598419
; Sequence 348, Application US/09598419
; Patent NO. 656586;
; Patent NO. 656586;
; Patent NO. 656586;
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; CURRENT FILING DATE: 2000-06-20
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 348
; LENGTH. 1464 1464 122 1 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-684-215B-23 (1-128) x US-09-598-419-348 (1-1464) ThrGlyAsnValThrLeuAlaGlu 128 121 ThrdlyAsnValThrLeuAlaGlu 128 TYPE: DNA;
; CRGANISM: Chlamydia trachomatis
US-09-598-419-348 6,96-59 608.00 96,09% 95,31% Percent Similarity: Best Local Similarity: SULT 29 -09-598-419-348 Alignment Scores: Pred. No.: 310 190 250 101 121 61 81 Query Match: DB: g a 8 8 ö 셤 ò g $\dot{\delta}$ g ò ઠે ò à g ð 원 상 점

```
250 Arcaccecedroacececrocarcaacroseceacecearesceares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 GlyHisHisBroGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 dedelahtartetededitakediteneredenearetiddeaaketaaditeddededaededi 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAG------CTTCCCACCGTTCAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProlle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGAATCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 Arcadacchaccacchichterragaratharcachacaccaacaacacacacaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 ileThralaValaspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1557
122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-23 (1-128) x US-09-620-412C-332 (1-1557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
RESULT 30
US-09-620-412C-332
US-09-620-412C-332
Sequence 332, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFI
FILE REFERENCE: 210121.4697C
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
SOFTWARE: FASESEQ for Windows Version 3.0/4.0
SEQ ID NO 332
LENGTH: 1557
TWOBEL DATE: DATE
THE TREE TREESED FOR WINDOWS OF THE TREESED FOR WINDOWS OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: April 30, 2004, 05:12:07 Job time: 713.531 seca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ThrGlyAsnValThrLeuAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 ACAGGGAACGTGACATTGGCCGAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA; Chlymadia trachomatis
US-09-620-412C-332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.486-59
608.00
96.09%
95.31%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 6 8 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

ACAGGGAACGTGACATTGGCCGAG 393

20 8 40 100

249

80

189

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/2/ina/5A COMB.seg:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seg:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seg:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seg:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seg:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seg:* Issued Patents NA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ID US-09-636-215-822 US-09-685-166A-822 US-09-736-457-1862	1	H 4 4 4	
US-09-643-597-0	4 4	9000	100.0 900 4
US-09-606-421B	4	900	900
US-09-636-215-6	4	915 4	100.0 915 4
US-09-685-166A	4	915 4	100.0 915 4
US-09-736-457-	4	945 4	100.0 945 4
US-09-643-597-	4	1012 4	100.0 1012 4
US-09-606-421B	4,	1012 4	1012 4
US-09-636-215-	4	1203 4	100.0 1203 4
US-09-685-166A	4	1203 4	100.0 1203 4

	Sequence 348, App	equence 332	equence 332	equence 188	188	188	equence 355	equence 352	equence 336	equence 336	equence 308	equence 306	eguence 324	equence 324	equence 316	316	340		326	356	31	37	347		35	326	equence 320	32	equence 27	equence 1,	quence 1,	6 5
US-09-620-412C-348	-09-598-419-34	-09-620-412C-3	-09-598-419-33	-09-556-877-18	-09-620-412C-1	-09-598-41	-09-620-412C-3	-09-598-419-35	-09-620-4120	-09-598-419-33	20-4120	19-598-419	39-620-412	19-598-419-32	19-620-412	19-598-419-31	39-620-412	39-598-419-34	39-620-412C-3	39-598-419-35	09-620-412	-09-598-41	-09-620-412C	-09-598-419-34	-09-620-412	-09-620-412C-32	09-598-419-	-09-598-419-32	-09-287-849-2	-09-223-04	S-09-287-849-1	-09-103-840
4,	4	4	4	4	4	4	4	4	4	4	4	4	4	4,	4	4	4	44	4	4	4	4	4	4	4	4	4	4	4	4,	4	m
1464	1464	53	55	57	57	1578	75	75	75	75	86	86	8	33	94	94	96	1965	5	8	5	5	2	음	7	7	7.	14	702	2287	2287	37
100.0	100.0	-	-	_	-		100.0															100.0					100.0			96.8		٠
653	653	in	10	ıΩ	£	653	ın	LO	n	TU.	ഥ	S	ហ	M	S	Ł	S	ഗ	ഗ	ß	ശ	വ	ഹ	വ	വ	വ	S	S	m	m	m	n
13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	8 C	6 6	40	41	42	43	44	4.5

ALIGNMENTS

US-09-636-215-822

| Sequence 822, Application US/09636215
| Patent No. 6620922
| GENERAL INFORMATION:
| APPLICANT: Xu, Jiangchun | APPLICANT: Dillon, Davin C. |
| APPLICANT: Mitchan, Jennifer L. |
| APPLICANT: Harlocker, Susan L. |
| APPLICANT: Handerson, Robert A. |
| APPLICANT: Retter, March B. |
| APPLICANT: Setter, Dary R. |
| APPLICANT: Banger, Gary R. |
| APPLICANT: Benger, Gary R. |
| APPLICANT: Benger, Gary R. |
| APPLICANT: Benger, William S. |
| APPLICANT: Hepler, William S. |
| APPLICANT: Hepler, William |
| TITLE OF INVENTION: DARGNOSITIONS AND METHODS FOR THE THERAPY AND |
| TITLE OF INVENTION: DARGNOSITIONS OF PROSTATE CANCER |
| TITLE OF INVENTION: DARGNOSITIONS OF SECURRENT PILICATION NUMBER: US/09/636,215 |
| CURRENT PILICATION NUMBER: US/09/636,215 |
| WUMBER OF SECUENCE 210121.4271717 |
| CURRENT PILICATION NUMBER: US/09/636,215 |
| NUMBER OF SECUENCE 210121.4271717 |
| TRANSTH' GARS FRANCE: 210121.4271717 |
| TRANSTH' RETER PRESENCE: 210121.4271717 |
| TRANSTH' RELICATION NUMBER: US/09/636,215 |
| TRANSTH' GARS FRANCE: 210121.4271717 |
| TRANSTH' RETER BERERE FRANCE: 210121.4271717 |
| TRANSTH' RELICATION NUMBER: US/09/636,215 |
| TRANSTH' RETER BERERE FRANCE: 210121.4271717 |
| TRANSTH' RETER FRANCE: 210121.42717 RESULT 1 US-09-636-215-822

Alignment Scores:

TYPE: DNA ORGANISM: Homo sapiens

```
141
                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                            261
                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                          40
                                                                                                                                               뛶
                                                                                                                                                                                                                           61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAepValIleThrAlaVal
202 GTCGGGAGCGCTCCGGCGGCAAGTCTCGACATCTCCACCGGCGACGTGTCATCACCGCGGTC
                                                                                                                      RESULT 2
US-09-685-166A-822
US-09-685-166A-822

US-09-685-166A-822

Sequence 822, Application US/09685166A

Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: Witcham, Jangohun C.
APPLICANT: Mitcham, Jannifer L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wang, Ailun
APPLICANT: Wang, Ailun
APPLICANT: Wang, Ailun
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
TITLE OF INVENTION: COMPOSITIONS AND TITLE OF INVENTION: UNMER: US/09/685,166A
CURRENT APPLICANT: 210121.427021
CURRENT APPLICANT: STOLE COMPUSED
SEQ ID NOS: 898
SOUTHARE FEATSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: AND
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                            US-09-684-215B-18 (1-128) x US-09-636-215-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                               1.06e-67
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Homo sapiens
US-09-685-166A-822
                 Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                         8 8
                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                     Š
                                                                                                                       δ
```

101 GlyaspvalileServalThrTrpGlnThrlysSerGlyGlyThrArgThrGlyAsnVal 120

à g

8 g

61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 202 GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC

8 S

261 100 321

80

201 9

22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC

g à ď ò 셤

ð

1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle

US-09-684-215B-18 (1-128) x US-09-685-166A-822 (1-675)

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

Score:
Score:
Score:
Farcent Similarity:
Best Local Similarity:
100.00\$
Ouery Match:
100.00\$

```
FOR THE THERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
00
00
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                  Sequence 1862, Application US/09736457
Sequence 1862, Application US/09736457
Sequence 1862, Application US/09736457
Sequence 1862, Application US/09736457
SERERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Panger, Cary
APPLICANT: Vedvick, Tom
APPLICANT: Retter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Ren, Liqum
APPLICANT: Ren, Liqum
APPLICANT: Ren, Liqum
APPLICANT: Wang, Aijum
APPLICANT: Wang, Aijum
APPLICANT: Wang, Aijum
APPLICANT: Ren, Liqum
APPLICANT: 
121 ThrLeuAlaGluGlyProProAla 128
                                                      382 ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.39e-67
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
US-09-736-457-1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
         ठे
```

Alignment Scores

ò

```
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261
                                                                                                                                                                                                                                                                                            81 AspGlyAlaProIleAsnSerAlaThrAlaWetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                           321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTAAC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                        81
                                                                                            9
                                                                                                                                                                                                                                                                                                                             262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyBheAlaileProile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ACGGCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                            41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-606-411B-353
; Sequence 353, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Fan, Liqun
; APPLICANT: Fan, Liqun
; APPLICANT: Fan, Cantanya S.
APPLICANT: Fanger, Chaitanya S.
APPLICANT: Hosken, Nancy
; APPLICANT: Hosken, Nancy
; APPLICANT: Hosken, Nancy
; APPLICANT: Hosken, Nancy
; APPLICANT: Applicant Stelly, Yasir A.W.
; APPLICANT: Mang, Aljun
; APPLICANT: Mang, Aljun
; APPLICANT: Stelky, Yasir A.W.
; APPLICANT: Stelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS
; TITLE OF INVENTION: COMPOSITIONS
; TITLE OF INVENTION: COMPOSITION
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; TITLE OF INVENTION: COMPOSITION
; TITLE OF INVENTION: AND MAGEN: US-09-606,421B
; NUMBER OF SEQ ID NOS: 356
; SEQ ID NO 333
; LENGTH: 900
; TIPE: DNA

TYPE: DNA

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-18 (1-128) x US-09-606-421B-353 (1-900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
Score:
Fercent Similarity:
Best Local Similarity:
Cuery Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $ 6 5 6 5
$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
松阳谷田谷田谷田谷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 141
                                                                                                                                                                                                                                                                                                                                                                                                      261
                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                              21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4

US-09-643-597-353

US-09-643-597-353

Sequence 353, Application US/09643597

Patent No. 6426072

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Ran, Liqun
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Mang, Aljun
APPLICANT: Modell, Patricia D.
APPLICANT: Mode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            900
1128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Gaps:
US-09-684-215B-18 (1-128) x US-09-736-457-1862 (1-822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-684-215B-18 (1-128) x US-09-643-597-353 (1-900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.58e-67
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-09-643-597-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score: 61
Percent Similarity: 11
Best Local Similarity: 11
Query Match: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                          142
                                                                                                                                                                                                                                                                                                                                                                                                            202
```

g

à

8 6 8 6 8 6 8 6 8

ઠે 셤

Db

8 6

ò 셤 ò g

```
201
                                                                                            100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                       101 GlyaspvalileServalThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                      40
                                                                                                                            262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAACGGGCATCAACCG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
                                             261
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCATTCGCATTCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProlle
                       202 GTCGGGAGCGCTCCGGCGCAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC
                                                                                               81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7

19-09-085-166A-0814

19-09-085-166A-0814

19-09-085-166A-0814

19-09-085-166A-0814

19-09-085-166A-0816

19-09-085-166A-0816

19-09-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215B-18 (1-128) x US-09-685-166A-834 (1-915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                              121 ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                           382 ACATTGGCCGAGGACCCCGGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.: 1.61e-67
Score: 653.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORDANISM: Homo sapiens
US-09-685-166A-834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                               ò
                                                                                                                                         임
                                                                                                                                                                                                    ठ
                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCGACGAGCGCACGAGTCCAACGGGTG 201
                                                                                                    81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                 101 GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
  321
                                                                                                                                    KESULY 6

KESULY 6

KESULY 6

KESULY 6

KESULY 6

KEGOSZ

KERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Mitcham, Janifer L.

APPLICANT: Mitcham, Janifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Robert A.

APPLICANT: Harlocker, Raral M.

APPLICANT: Harlocker, Raral M.

APPLICANT: Rades, Michael D.

APPLICANT: Rades, Michael M.

APPLICANT: Rades, Michael M.

APPLICANT: Rades, Michael M.

APPLICANT: Stolk, John A.

APPLICANT: Gary R.

APPLICANT: Gary R.

APPLICANT: Wang, Aijun

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Beleler, William

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE

CURRENT APPLICATION NUMBER: US/09/636,215

CURRENT FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 852

SOFTWARE: FastSEQ for Windows Version 3.0

LEMTH: NUMBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            915
0 0 0
0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-684-215B-18 (1-128) x US-09-636-215-834 (1-915)
                                                                                                                                                                                                                                                                                                   121 ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.61e-67
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
, ORGANISM: Homo sapiens
US-09-636-215-834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142
                                                                                                                                                         262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .. oN
```

g 8

 δ g 8 us-09-684-215b-18.rni

```
ThrLeuAlaGluGlyProProAla 128
                                                                                         121 ThrLeuAlaGluGlyProProAla 128
                                                                                                                            382 ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
Score:
Score:
Bercent Similarity:
Best Local Similarity:
100.00$
Dery Match:
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CRGANISM: Homo sapiens
US-09-643-597-351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>a</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ሪ 8 ሪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                         ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141
100
                                                                                                                                                101 GlyAspVall1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                        80
                                                                                             262 GACGGCGCTCCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVallleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACGGCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlyGlnalaMetalaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                         AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               945
128
0
0
0
                                                                                                                                                                                                                                                                                              RESULT 8

US-09-736-457-1861

Sequence 1861, Application US/09736457

Patent No. 650948

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Panger, Garry
APPLICANT: Tonger, Garry
APPLICANT: Retter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Pan, Liqun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
SPELICANT: Wang, Aijun
APPLICANT: Wannion, Jane
APPLICANT: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-18 (1-128) x US-09-736-457-1861 (1-945)
                                                                                                                                                                                                                           1.69e-67
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202
                                                                         81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 & 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          장염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $ G
                              엄
                                                                 8 8 8
                                                                                                                                                                                셤
                                                                                                                                                                                                                           δ
```

```
186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 GlyAspVall1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426
                           381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 ACGCCCCCCCCCATAACTICCAGCTCTCCCAGGCTGGCCAGGCATTCCCATTCCCATC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 GCCTTCCTCGGCTTGGGTGTTGTCGACACACGGCAACGGCGCACGAGTCCAACGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 GGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGGGGGCAGCGCGTGAAAGGTG
                       41 AlaPheLeuGlyVeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
101 GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ThrAla&laSerAspAsnPheGlnLeuSerGlnGlyGlyGlyPheAlaIleProlle
                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE THERAPY
                                                                                                                                       RESULT 9

US.-09-64-597-351

Sequence 351, Application US/09643597

Sequence 36426072

Datent No. 6426072

GENERAL INFORMATION:
APPLICANT: Wang, Liqun
APPLICANT: Rale, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Hosken, Nancy
APPLICANT: Wang, Ajun
APPLICANT: Hosken, Nancy
APPLICANT: Washir A.W.
APPLICANT: Washir A.W.
APPLICANT: Skelky, Yashir A.W.
APPLICANT: Skelky, Yashir A.W.
APPLICANT: Skelky, Yashir A.W.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
TITLE OF INVENTION: COMPOSITIONS
CURRENT PILING DATE: 2000-08-21

CURRENT PILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 369

SOFTWARE: RateSeQ for Windows Version 3.0

SEQ ID NO 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-18 (1-128) x US-09-643-597-351 (1-1012)
```

```
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                          APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisFro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyaspvalileServalThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnval 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 defidacercarcricedreaccreecaaaccaaerceeececacecacecaaceeaacere 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 ACGCCCCCCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 GIGGGAAGGGTCCGGGGGGGAAGTCTCGGCATCTCCACCGGGGACGTGATCACCGCGGTT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 GACGGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAACGGGCATCATCCC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACGTTCATATCGGGCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ThralaalaSeraspaspheGlnLeuSerGlnGlyGlyGlnGlyPheAlaileProile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 GCCTTCCTCGGCTTGGGTGTTGTCGACAACGACGGCAACGGCGCACGAGTCCAACGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                          Sequence 351, Application US/09606421B

Sequence 351, Application US/09606421B

Sequence 351, Application US/09606421B

Setent No. 6531315

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Ralos, Michael D.

APPLICANT: Fanger, Chaitanya S.

APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

APPLICANT: Samuel X.

APPLICANT: Samuel X.

APPLICANT: Semuel X.

APPLICANT: Find X.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-684-215B-18 (1-128) x US-09-606-421B-351 (1-1012)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrLeuAlaGluGlyProProAla 128
427 ACATTGGCCGAGGACCCCCGGCC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-636-215-851
Sequence 851, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.85e-67
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-09-606-421B-351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
101 GlyaspvalileservalThrirpGlnThriysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 GGGCAGGCGATGGCGGATCGGCCAGGCTTCCCACGTTCATATCGGGCCTACC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ACGGCCGCGTCCCGATAACTICCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValileThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProlle
                                                                                                                                                                                                                                                                                                                                        ODS FOR THE THERAPY AND CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-18 (1-128) x US-09-636-215-851 (1-1203)
                                                                                                                                                                                                                                                                             APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF EDG ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SSEQ ID NO 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-685-166A-851
; Sequence 851, Application US/09685166A
; Patent No. 6630305
; GBNERAL INFORMATION:
Xu, Jiangcmun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Ralos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        653.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA; CRGANISM: Homo sapiens US-09-636-215-851
```

261 100 321

80

201 9

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Sunnifer L.
APPLICANT: Harlocker, Sunnifer L.
APPLICANT: Harlocker, Nobert A.
APPLICANT: Raines, Michael D.
APPLICANT: Retter, Mare M.
APPLICANT: Retter, Mare M.
APPLICANT: Retter, Mare M.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Li Samuel
APPLICANT: Usamuel
APPLICANT: Wang, Aijun
APPLICANT: Mang, Aijun
APPLICANT: Mang, Aijun
APPLICANT: Mang, Aijun
APPLICANT: Mang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Mang, Aijun
APPLICANT: Mang, Aijun
APPLICANT: William
ITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT FILING DATE: 2000-10-10
CURRENT FILING DATE: 2000-10-10
SOFTWARE: PESESEQ for Windows Version 3.0
SEQ ID NO 851
LENGTH: 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.34e-67
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-09-685-166A-851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
```

81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100 GlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120 261 GACGGCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC 321 82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGCCTACC 141 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 382 ACATTGGCCGAGGACCCCCGGCC 405 ThrieuAlaGluGlyProProAla 128 262 101 121 g g δ g ò 셤 g ઠે a ઠે 8 Š 유 Š

40

20 18

US-09-684-215B-18 (1-128) x US-09-685-166A-851 (1-1203)

RESULT 13
US-09-620-412C-348
Sequence 348, Application US/09620412C
Parent No. 6448234
GENERAL INFORMATION:

141 201 261 81 AspGlyAlaProlleAsnSeralaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100 321 80 87 40 9 22 ACGGCCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGCCAGGGATTCGCCATTCCGATC 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 202 GICGGGAGCGCTCCGGCGGCAAGICTCGGCATCTCCACCGGCGACGTGATCACCGGGGTC 262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCCTTAACGGGCATCATCCC 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: PASISEQ for Windows Version 3.0/4.0
SEQ ID NO 348
LENGTH: 1464 US-09-684-215B-18 (1-128) x US-09-620-412C-348 (1-1464) Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 121 ThrLeuAlaGluGlyProProAla 128 382 ACATTGGCCGAGGACCCCCGGCC 405 ; TYPE: DNA ; ORGANISM: Chlamydia trachomatis US-09-620-412C-348 3.07e-67 653.00 100.00% 100.00% Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.: g ò g g à g 8 ઠ

RESULT 14
US-09-598-419-348
US-09-598-419-348
; Sedent No. 656886
; GARERAL INFORMATION:
 APPLICANT: Scholler, John
 TITLE OF INVENTION:
 TITLE OF INVENTION:
 TITLE OF INVENTION: COMPOUNDS ND METHODS FOR TREATMENT AND TITLE OF INVENTION: OF CORRENT APPLICANTION: OF CORRENT PRILOR DATE: 2000-06-0; CURRENT FILING DATE: 2000-06-0; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 348
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-598-419-348

Alignment Scores

```
201
                                                                                                                                                                                                                                                                                                         100
                                                                                                                                                                                                                                                                                                                                                                                    262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
                                                                                                                                                                                                             82 GGGCAGGCGATGGCGATCGCGGGCCAAGCTTCCCACCGTTCATATCGGGCCTACC 141
                                                                                                                                                                                                                                                                                                                                                                                                                               101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                            81
                                                                                                                                                  22 ACGGCCGCGTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                          21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLySLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                  81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 ACGCCGCCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                    1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Steven P. Fling
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
ITILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPERENCE: 210121-44697
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FRASESEQ for Windows Version 3.0/4.0
SEQ ID NO 332
LENGTH: 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1557
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-18 (1-128) x US-09-620-412C-332 (1-1557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                     US-09-684-215B-18 (1-128) x US-09-598-419-348 (1-1464)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ThrheuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 332, Application US/09620412C Patent No. 6448234 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Chlymadia trachomatis
US-09-620-412C-332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.348-67
653.00
100.00%
100.00%
3.07e-67
653.00
100.00%
100.00%
                         Percent Similarity:
Best Local Similarity:
Query Match:
D8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
Percent Similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-09-620-412C-332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                        g
                                                                                                                                                                                           ò
                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                        8 8
                                                                                                                                                                                                                                                                                                                                                           ò
```

```
102 GTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGGTC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 Glyaspvall1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 gacgecercogarcaacregeceaceaegargeceaegaceceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargeceargecea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 doscadocarroscoarcecedeceaercanderrecencearcararecedeceraec 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ValGlySerAlabroAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlyGhealaileProile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ACGGCGCGCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                        US-09-588-419-332

Sequence 332, Application US/09598419

Patent No. 656856

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Scholler, John

ITTLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

FILE REFERENCE: 210121-469C6

CURRENT APPLICATION NUMBER: US/09/598,419

CURRENT FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 357

SOFTWARE: FastSEQ for Windows Version 3.0/4.0

SEQ ID NO 33.2

LENGTH 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-18 (1-128) x US-09-598-419-332 (1-1557)
382 ACATIGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Chlymadia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.34e-67
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-598-419-332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . No. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
          셤
```

101 GlyAspVallleSerValThrTrpGlnThrlysSerGlyGlyThrArgThrGlyAsnVal 120

121 ThrieuAlaGluGlyProProAla 128

& g

g S a

ö

ò

41 AlaPhereuGlyTeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal

81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100 101 GlyAspVall1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120 GACGGCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC 321 82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 141 142 GCCTTCCTCGGCTTGGGTGTTGTCGACAACGACAACGGCGCACGAGGTCCAACGGCGT 201 9 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80 GGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGTACAGGGAACGTG 381 20 81 40 22 ACGGCCCCCGTCCCGATACTTCCCACTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC GlyGlnAlaMetAlaileAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle Sequence 188, Application US/09556877

Sequence 188, Application US/09556877

Patent No. 6432916

GENERAL INFORMATION:
APPLICANT: Probst, Peter
APPLICANT: Skeiky, Yasir
APPLICANT: Fling, Steve
APPLICANT: Fling, Steve
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.46595

CURRENT APPLICATION NUMBER: US/09/556,877

CURRENT FILING DATE: 2000-04-19

NUMBER OF SEQ ID NOS: 305

SEQ ID NO 188

LENGTH: 1578

MANDE: NANA

LENGTH: 1578

MANDE: NANA

LENGTH: 1578

LENGTH: 1578

LENGTH: 1578 1578 128 0 0 0 Length:
Matches:
Conservative:
Mismatches: US-09-684-215B-18 (1-128) x US-09-556-877-188 (1-1578) 121 ThrLeuAlaGluGlyProProAla 128 382 ACATTGGCCGAGGGACCCCCGGCC 405 121 ThrLeuAlaGluGlyProProAla 128 382 ACATTGGCCGAGGGACCCCCGGCC 405 Sequence 188, Application US/09620412C Patent No. 6448234 GENERAL INFORMATION: 3.4e-67 653.00 100.00% 100.00% APPLICANT: Steven P. Fling Alignment Scores:
Pred. No.:
Score:
Fercent Similarity:
Dest Local Similarity:
Ouery Match:
DB: TYPE: DNA CRGANISM: Chlamydia US-09-556-877-188 RESULT 18 US-09-620-412C-188 RESULT 17 US-09-556-877-188 262 н 21 41 19 202 322 g δ 엄 g ò g 8 임 à a ò d ò δ g 8 8

```
82 GGGCAGGCGATGGCGATTCGGATCGCGGCCAATTCAAACTTCCACCGTTCATATCGGGCCTACC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 GICGGGAGGGTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTGATCACGCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ValGlySerAlaProAlaAlaSerLeuGlylleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                       1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REPERENCE: 210121.446507
CURENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: PEAGESEQ for Windows Version 3.0/4.0
SEQ ID NO 188
LENGTH. 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TREATMENT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 19
US-09-598-19-188
Sequence 188, Application US/09598419
Fatent No. 6565856
GENERAL INFORMATION:
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT A. TITLE OF INVENTION: DAGNOSURS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121.46906
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE FALLING DATE: 2000-06-20
SOFTWARE FALLING DATE: Almows Version 3.0/4.0
SEQ ID NO 188
SEQ ID NO 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1578
                                                                                                                                                                                                                                               1578
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-18 (1-128) x US-09-620-412C-188 (1-1578)
                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ThrieuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                 653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Chlamydia
                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                            TYPE: DNA
, ORGANISM: Chlamydia
US-09-620-412C-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                        .. oN .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 6 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
202 GTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC 261
                                                                                                                                                                                                                                                                                                                                                                                                            262 GACGGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAACGGGCATCATCATCCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 GlyaspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
                                                                                                                                                                                                                                                                                                                         61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVallleThrAlaVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                             1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                  22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGCTGGGCAGGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 352, Application US/09620412C

Sequence 352, Application US/09620412C

Patent No. 6448234

GENERAL INFORMATION:

APPLICANT: Steven P. Fling

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

CURRENT APPLICATION NUMBER: US/09/620,412C

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363

SOFTWARE: FastSEQ for Windows Version 3.0/4.0

SEQ ID NO 352

LENGTH: 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1752
128
0
0
0
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-18 (1-128) x US-09-620-412C-352 (1-1752)
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                              US-09-684-215B-18 (1-128) x US-09-598-419-188 (1-1578)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 ACATTGGCCGAGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.92e-67
653.00
100.00%
100.00%
653.00
100.00%
100.00%
               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-620-412C-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Chla
US-09-620-412C-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 20
US-09-620-
                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                               요
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                             ð
                                                                                                                                                        d
                                                                                                                                                                                     ò
                                                                                                                                                                                                                       원
                                                                                                                                                                                                                                                 \dot{\delta}
                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

 S 6	322					4 t
 3	9		ורשורורמפופשריו	999719447744499		
 පි පි	121 382		ThrieuAlaGluGlyProProAla 	1a 128 CC 405		
RESULT 21 US-09-598-4 Sequence Sequence Settler GENERAL I APPLICAN TITLE OF TITLE OF TITLE OF TITLE OF CURRENT CURRENT CURRENT SOFTWARE SOFTWARE SOFTWARE SOFTWARE TITLE	ULT 21 09-598-419-352 equence 352, 352 equence 352, 362 ENERAL INFORMAT APPLICANT: SKEIL AP	SULT 21 -09-598-419-352 Sactent No. 556.885 GENERAL INFORMATION: APPLICANT: SKelfy, Yas APPLICANT: SKelfy, Yas APPLICANT: SKelfy, Yas TITLE OF INVENTION: CO FILE REFERENCE: 210121 FILE REFERENCE: 210121 CURRENT FILING DATE: 2 SUSTWARE: FastSEQ for SEQ ID NOS: 2 SEQ ID NO 352 LENGTH: 1752 TYPE: DNA ORGANISM: Chlamydia t -09-598-419-352	ation US/09598 Yasir A.W. John COMFOUNDS AND 121.469C6 NUMBER: US/09: 1.2000-06-20 S: 357 or Windows Ver	9 ETHODS FOR 98,419 on 3.0/4.0	TREATMENT AND PECTION	
 Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	nt Scores: o.: Similarity cal Similar atch:	cores: nlarity: Similarity ::	3.92e-67 653.00 100.00\$: 100.00\$ 4	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1752 128 0 0 0	
 US-09-684-215B-18	84-215		(1-128) x US-09-598	8-419-352 (1-1752	~	
 çy Qa	1 22		laSerAspAsnPheG cGrccsarAacrrcc	ThralaalaSerAspasnPheGlnLeuSerGlnGlyGly 	ThralaalaseraspasphedinleuserdinglydinglyghealaileProile 	20
 yo da	21		laMetAlaileAlaG GATGGCGATCGCGG	lyGlnileLysLeuPro 	GlyglnalametalarlealaglyglnrletysLeuproThrvalHisrleglyProThr 	40
 දු දු	41		euGlyLeuGlyValV TCGGCTTGGGTGTTG	alaspasnasnGlyasi TCGACAACAACGGCAA	AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 	60
 Oy Qa	61		erAlaProAlaAlaS 	erLeuGlylleserth: 	ValGlySerAlabroAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 	80
 Q7 Dp	81		laProlleAsnSerA 	aThralaMetalaAs 	AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisFiro 	321
 8 %	101		alileSerValThrT [TCATCTCGGTGACCT	rpGlnThrLysSerGl; GGCAAACCAAGTCGGG	GlyaspvalileServalThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnval 	381

101 GlyAspVall1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120

> g δ

8 8 8 8

41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal

101 GlyAspvall1eServalThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120 202 GICGGGAGCCTCCGGCGCCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGGCGGTC 261 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80 20 81 22 ACGGCCCCCCCCCCATAACTTCCCAGCTGTCCCAGGGTGGCCAGGGATTCGCCATTCCCATC 1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlalleProlle ; Sequence 336, Application US/09620412C
; Batent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7;
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTHARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 336
; LENGTH: 1758 Sequence 336, Application US/09598419
Patent No. 6565856
GENERAL INFORMATION:
APPLICANT: Skeliky, Yasir A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.46506
CURRENT APPLICATION NUMBER: US/09/598,419 US-09-684-215B-18 (1-128) x US-09-620-412C-336 (1-1758) Length:
Matches:
Conservative:
Mismatches:
Gaps: 121 ThrLeuAlaGluGlyProProAla 128 382 ACATTGGCCGAGGGACCCCCGGCC 405 , TYPE: DNA , ORGANISM: Chlymadia trachomatis US-09-620-412C-336 3.94e-67 653.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: DB: RESULT 23 US-09-598-419-336 US-09-620-412C-336 Alignment Scores: Pred. No.: Score: ठ g ò QQ g δ g ò g ∂ g δ ద ò g

```
141
                                                                                                                                                                                                                                  201
                                                                                                                                                                                                                                                                                261
                                                                                                                                                                                                                                                                                                         100
                                                                                                                                                                                                                                                                                                                               321
                                                                                                                                                                                                                                                                                                                                                                             381
                                                                                                                                                                                                          9
                                                                                                                                81
                                                                                                                                                             40
                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                        101 GlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                                                                                                            22 ACGGCCGCGTCCGATAACTICCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCGATC
                                                                                                                                                             61 ValGlySeralaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                            202 GTCGGGAAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC
                                                                                                                                                                                                                                                                                                                                                                     1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaileProile
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 24
US-09-620-412C-308
US-09-620-412C-308
; Sequence 308, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
    APPLICANT: Steven P. Fling
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
    TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
    FILE REPRENNIE: 2.10121.46977
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOPTUARE: FASESEQ for Windows Version 3.0/4.0
; SEQ ID NO 308
; LENGTH: 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11860
2860
0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
       Length:
Matches:
Conservative: (
Mismatches:
                                                                                       US-09-684-215B-18 (1-128) x US-09-598-419-336 (1-1758)
                                                                                                                                                                                                                                                                                                                                                                                                        121 ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                      382 ACATTGGCCGAGGACCCCCGGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.25e-67
653.00
100.00%
100.00%
       3.94e-67
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
Alignment Scores:
            Pred. No.:
                        Score:
                                                                                                                                                                                                                                                             8 8 8
                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                        엄
                                                                                                                                                            ठ
                                                                                                                                                                                    음
                                                                                                                                                                                                                                d
                                                                                                                   ઠે
                                                                                                                                                                                                         ⋧
```

CURRENT FILING DATE: 2000-06-20 NUMBER OF SEQ ID NOS: 357 SOFTWARE: FREISEQ FOR Windows Version 3.0/4.0 LENGTH: 1758

TYPE: DNA ORGANISM: Chlymadia trachomatis

; OKGANISM: CDI US-09-598-419-336

```
61
                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
            8 & 8
                                                                       8 8
                                                                                                         Š
                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCTTCCTCGGCTTGGGTGTTGTCGACACAACAACGGCAACGGCGCACGAGTCCAACGGCGTG 201
                                                                                                                                                                                100
                                                              201
                                                                                                                                                             261
                                                                                                                                                                                                   321
                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                GlyGlnAlaMetAlaIleAlaGlyGlnIleLySLeuProThrValHisIleGlyProThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 ACGGCCGCGTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGAATTCGCCATTCCGATC 81
                                                                                                     9
                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                             81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                    81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                         GlyAspValIleSerValThrTpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                       ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                            ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                             Sequence 308, Application US/09598419
; Sequence 308, Application US/09598419
; Patent No. 6565856
; GRNERAL INFORMATION:
; APPLICANT: Schooller, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.46966
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 308
; LENGTH: 1860
; TENGTH: 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1860
128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Gaps:
          US-09-684-215B-18 (1-128) x US-09-620-412C-308 (1-1860)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-18 (1-128) x US-09-598-419-308 (1-1860)
                                                                                                                                                                                                                                                           ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                      382 ACATTGGCCGAGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA Chlamydia trachomatis US-09-598-419-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.25e-67
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                   RESULT 25
US-09-598-419-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142
                                                                                                                                                              202
                                                                                                                                                                                                    262
                                                                                                                                                                                                                       101
                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                       $ g
                                                                                                                                                                                                                                                       ò
                           8 6 6
                                                                                유 상 유
                                                                                                                                       8 8 8
                                                                                                                                                                                              엄
```

```
141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381
                                                               100
                                                                                       262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                             261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGGCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAsaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 GCCTTCCTCGGCTTGGGTGTTGTCGACACACGGCAACGCGCACGAGTCCAACGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 dacedecicricearcaacredecacedeardecedacedecerraacedecareareee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyAspVallleSerValThrTrpGlnThrLy8SerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaileProlle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 ACGGCCGCGTCCCGATAACTTCCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                       202 Greggagegerecegegeaagreteggaatereeagegagegaegreategegee
                                                             AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVallleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                          FOR TREATMENT AND INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1896
1128
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-684-215B-18 (1-128) x US-09-620-412C-324 (1-1896)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                           Sequence 324, Application US/09620412C

Patent No. 6448234
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFE
FILE REFERENCE: 210121.4697
CURRENT APPLICATION NOWBER: US/09/620,412C
CURRENT APPLICATION NOWBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 324
LENGTH: 1896
TYPE: DNA
ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                   121 ThrieualaGluGlyProProAla 128
182 ACATTGGCCGAGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.37e-67
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
Score:
Percent Similarity:
Dest Local Similarity:
Ouery Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Chlan
US-09-620-412C-324
                                                                                                                                                                                                                                                                        RESULT 26
US-09-620-412C-324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382
                                                                   81
```

```
81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 GACGGGGTCCGATCAACTCGGCCACGGGATGGCGGACGCGCTTAACGGGCATCATCCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 GTCGGGAGGCGTCCGGCAGGAGTCTCGGCATCTCCACCGGCGACGTGATCACGGCGTC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 ACGGCGCGTCCCAATACTTCCAGCTGTCCCAGGGTGGCAGGATTCCCATTCCCATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLySLeuProThrValHisIleGlyProThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Sequence 316, Application US/09620412C
| Patent No. 6446234
| GENERAL INFORMATION:
| APPLICANT'S feeven P. Fling
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
| TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
| TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
| FILE REPERSENCE: 210121.46967
| CURRENT PILING DATE: 2000-07-20
| NUMBER OF SEQ ID NOS: 363
| SOFTWARE: FastSEQ for Windows Version 3.0/4.0
| SEQ ID NO 316
| LENGTH: 1941
Sequence 324, Application US/09598419
; Sequence 324, Application US/09598419
; Patent No. 656586
; GENERAL INPORMATION:
    APPLICANT: Scholler, John No. 7
    APPLICANT: Scholler, John No. 7
    TITLE OF INVENTION: COMPONIOS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
    TITLE OF INVENTION: 357
    CURRENT APPLICATION NUMBER: US/09/598,419
    CURRENT PILING DATE: 2000-06-20
    SOFTWARE: PastesEQ for Windows Version 3.0/4.0
    SEQ ID NO 324
    LENGTH: 1896
    TYPE: DNA
    TYPE: DNA
    CORDANISM: Chlamydia trachomatis
    US-09-598-419-324
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-18 (1-128) x US-09-598-419-324 (1-1896)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                 4.37e-67
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity: 1
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 28
US-09-620-412C-316
                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
```

Alignment Score Pred. No.: Secret: Sec	Scores: Similarity: Similarity: Similarity: Thralable Thralable Collyginals Right	4.51e-67 653.00 100.00\$ 100.00\$ 100.00\$ 4 28) x US-09-620 aSerAspAsnPheGli GIT	### 1941 ### 1516-67		20 81 40 60 60 201
6 6 6 6 6			anhralametalaasp 	0-U H-U	100 321 120 381
NESULT 29 US-09-598-419- Sequence 316 Patent No. 6 GENERAL INFO APPLICANT: TITLE OF INF TITLE OF INF FILE REPERE CURRENT FILE CURRENT FILE SEQ ID NO 31 LENGTH: 19 LE	SULT 29 -09-598-419-316 -09-598-419-316 Patent No. 656586 GENERAL INFORMATION: APPLICANT: SKelky, Yasir APPLICANT: Skelky, Yasir APPLICANT: Scholler, John TITLE OF INVENTION: OMPOR FILE REPERNOE: 210121.46 CURRENT APPLICATION NUMBER CURRENT FILING DATE: 2000 NUMBER OF SEQ ID NOS: 357 SOFTWARE: FastSEQ for Min SEQ ID NO 316 LENGTH: 1941 TYPE: DNA ORGANISM: Chlamydia trac	US/09598 A.W. COSIS OF OSIS OF COSIS OF	419 METHODS FOR TREATMENT CHLAMYDIAL INFECTION /598,419 /sion 3.0/4.0	TMENT AND	
 Alignment S. Pred. No.: Score: Percent Sim Best Local Query Match DB:	nment Scores: . No.: ent Similarity: Local Similarity: Y Match:	4.51e-67 653.00 100.00% 100.00% 4	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1941 128 0 0 0	
 US-09-684-215B Qy 1 '	-215B-18 (1-1 1 ThrAlaAl	-128) x US-09-598 AlaSerAspAsnPheGl	8-419-316 (1-194) InLeuSerGlnGlyGly	-18 (1-128) x US-09-598-419-316 (1-1941) ThralaalaSerAepAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlarleProlle 1	50

; TYPE: DNA ; ORGANISM: Chlamydia trachomatis US-09-620-412C-316

81 ASPGIYALaProlleAsnSerAlaThrAlaWetAlaAspAlaLeuAsnGlyHisHisPro 100 101 GlyAspVall1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120 261 262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGACGCGCTTAACGGGCATCATCCC 321 GGGCAGGCGATGGCGATCGCGGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 141 80 40 81 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 202 GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC ACGCCCCCCCCCCATAACTTCCCACTGTCCCAGGGTGGGCAGGGATCGCCATTCCGATC 21 GlyGlnAlaMetAlaileAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 셤 ò g ਨੇ ò g 8 g δ q à

RESULT 30
US-09-620-412C-340
is-quence 340, Application US/09620412C
sequence 1NVEMATION:
TITLE OF INVEMATION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVEMATION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVEMATION: DIAGNOSIS OF CHLAMYDIAL INFECTION
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 340
INFERTING THE SECOND SEQ ID NOS: 363
SOFTWARE: Assumption trachomatics
US-09-620-412C-340

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 4.59e-67 653.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.:

US-09-684-215B-18 (1-128) x US-09-620-412C-340 (1-1965) ò

쉱

ద ò

ઠે

 \ddot{o}

20

81

41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal

AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100

101 GlyAspVallleSerValThrTrpGlnThrIysSerGlyGlyThrArgThrGlyAsnVal 120 262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCT ThrieuAlaGluGlyProProAla 128 382 ACATTGGCCGAGGACCCCCGGCC 405 121 음 중 음 ò ď

Search completed: April 30, 2004, 05:01:19 Job time : 76.5311 secs

ĕ

```
61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
317, App
341, App
341, App
341, App
357, App
313, App
313, App
345, App
345, App
329, App
321, App
321, App
321, App
329, App
329, App
329, App
320, App
321, App
321, App
321, App
322, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGTRTGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAASDNFQLSQGGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
      seduence sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE THERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 1e-67;
Matches 128; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, Jangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Handerson, Robert A.
APPLICANT: Fanger, Marc M.
APPLICANT: Fanger, Marc M.
APPLICANT: Fanger, Marc M.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc M.
APPLICANT: Carter, Marc M.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: APPLICANT: Carter, Darrick
APPLICANT: APPLICANT: Carter, Darrick
APPLICANT: Mang, Aijun
APPLICANT: Mang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Walliam
APPLICATION WUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
LUBRGTH: 224
LENGTH: 224
LENGTH: 224
LENGTH: 224
LENGTH: 224
LENGTH: 224
US-09-620-412-317
US-09-598-413-317
US-09-598-419-341
US-09-620-412C-341
US-09-598-410-357
US-09-598-410-357
US-09-598-410-313
US-09-598-410-313
US-09-598-410-313
US-09-598-410-329
US-09-598-419-329
US-09-598-419-329
US-09-598-419-329
US-09-598-419-329
US-09-598-419-329
US-09-598-419-329
US-09-287-640-2
US-09-287-640-2
US-09-287-640-2
US-09-287-640-2
US-09-287-640-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-09-636-215-825
US-09-636-215-825
PACHORO BOSD, Application US/09636215
PACHOL NO. 6620922
GENERAL INFORMATION:
APPLICANT:
APPLICANT
            TYPE: PRT
CRGANISM: Homo sapiens
US-09-636-215-825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLAEGPPA 135
         н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128
         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 825, Agequence 825, Agequence 825, Agequence 832, Agequence 1864, Agequence 835, Agequence 835, Agequence 835, Agequence 835, Agequence 835, Agequence 835, Agequence 849, Agequence 349, Agequence 349, Agequence 349, Agequence 349, Agequence 196, Ageque
                                                                                                                                                                                                        April 20, 2004, 06:21:52; Search time 22 Seconds (without alignments) 300.369 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              653
1 TAASDNFQLSQGGQGFAIPI.....QTKSGGTRTGNVTLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued Patents AA:*

1. \cgn2_6/ptodard2/iaa/5A_COMB.pep:*
\cgn2_6/ptodard2/iaa/5B_COMB.pep:*
3: \cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
4: \cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: \cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
6: \cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*
6: \cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*
                                    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-636-215-825

US-09-643-597-352

US-09-664-21B-352

US-09-666-421B-352

US-09-666-421B-352

US-09-666-421B-354

US-09-666-421B-354

US-09-666-421B-354

US-09-666-421B-354

US-09-668-115-852

US-09-658-116-852

US-09-658-116-852

US-09-620-412C-333

US-09-598-419-196

US-09-598-419-196

US-09-598-419-196

US-09-598-419-196

US-09-598-419-196

US-09-598-419-337

US-09-598-419-337

US-09-620-412C-333

US-09-620-412C-333

US-09-598-419-337

US-09-620-412C-337

US-09-620-412C-337

US-09-620-412C-337

US-09-620-412C-337

US-09-620-412C-337

US-09-620-412C-337

US-09-620-412C-325

US-09-620-412C-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                         US-09-684-215B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                  Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  %
Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB E
Maximum DB E
                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
No.
                                                                                                                                                                                                              Run on:
```

ö

9 67

```
61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWOTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 VGSAFAASLGISTGDVITAVDGAPINSATAMADALNGHHFGDVISVTWQTKSGGTRIGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TAASDNFQLSQGGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 352
LENGTH: 267
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 128; Conservative
                                                                                                                                                                                                           TYPE: PRT
CAGANISM: Homo sapiens
US-09-643-597-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-606-421B-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TAASDNFOLSOGGOGFAIPIGQAMAIAGOIKLPTVHIGPTAFLGLGVVDNNGNGARVORV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Retuer, Marcy
APPLICANT: Retuer, Marcy
APPLICANT: Retuer, Marcy
APPLICANT: Retuer, Mohn A.
APPLICANT: Carlot, John A.
APPLICANT: Carlot, John A.
APPLICANT: Darick
APPLICANT: Darick
APPLICANT: Li Samuel
APPLICANT: Li Samuel
APPLICANT: Li Samuel
APPLICANT: Mang, Aljun
APPLICANT: Alju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 653; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 1e-67;
Matches 128; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C11
                                                                                                                                           Sequence 825, Application US/09685166A
Patent No. 6630305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 352, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
                                                                                                                                                                                                           APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Jensen G.
APPLICANT: Carter, Jensen G.
APPLICANT: Li, Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Warg, Tongtong
Fan, Ligun
Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-09-685-166A-825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-643-597-352
                                                                                                                            US-09-685-166A-825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

ö

Gaps ö

Length 267; 0; Indels

100.0%; Score 653; DB 4; 100.0%; Pred. No. 1.3e-67; trive 0; Mismatches 0;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 VGSAPAASLGISTGDVITAVDGAPINSATAWADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Ran, Ligun
APPLICANT: Ran, Ligun
APPLICANT: Ranger, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF TITLE CANCER
TITLE OF TITLE CANCER
TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

100.0%; Score 653; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                    Sequence 352, Application US/09606421B Patent No. 6531315 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRGANISM: Homo sapiens
US-09-606-421B-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TLAEGPPA 128
128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-09-736-457-1864
```

```
Best Local Similarity 100.0%; P
Matches 128; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-09-606-421B-354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                       128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                         121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                             임
                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRIGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TAASDNFQLSQGGQGFAIFIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 TAASDNFQLSQGGGGFAIPIGQAMAIAGQIKLPTVHIGFTAFLGLGVVDNNGNGARVQRV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                         APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chattanya S.
APPLICANT: Bangur, Chattanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Panger, Gary
APPLICANT: Panger, Gary
APPLICANT: Retter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Fang, Aijun
APPLICANT: Fang, Aijun
APPLICANT: Pang, Aijun
APPLICANT: Pang, Aijun
APPLICANT: Wang, Aijun
APPLICANT
APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 100.0%; Score 653; DB 4; Length 273 Best Local Similarity 100.0%; Pred. No. 1.4e-67; Matches 128; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 653;
   Sequence 1864, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPCDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                       61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                  68 VGSAPASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TAASDNEQLSQGGGGGAAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                      8 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-60-60-421B-354
) Sequence 354, Application US/09606421B
) Sequence 354, Application US/09606421B
) Patent No. 6531315
) GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
) APPLICANT: Ralos, Michael D.
APPLICANT: Fan, Liqun
APPLICANT: Fanger, Gary R.
APPLICANT: Samuel X.
                                                ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Score 653; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 1.5e-67;
Matches 128; Conservative 0; Mismatches 0; Indels
Pred. No. 1.5e-67;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASOUT 0. 626-215-835
Sequence 835, Application US/09636215
Fatent No. 6620922
GENERAL INFORMATION:
APPLICANT: ALILON, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Suean L.
APPLICANT: Harlocker, Suean L.
APPLICANT: Handerson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Fanger, Gary R.
```

```
61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                               APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TILE REFERENCE: 210121.42717C17
CURRENT APPLICATION UNDER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FeastSEQ for Windows Version 3.0
SEQ ID NO 835
LENGTH: 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 835, Application US/09685166A

Batent No. 6630305

GENERAL INFORMATION

APPLICANT: Xu, Jiangchun

APPLICANT: Xu, Jiangchun

APPLICANT: Alangchun

APPLICANT: Henderen, Robert A.

APPLICANT: Henderen, Robert A.

APPLICANT: Fanger, Gary R.

APPLICANT: Fetter, Marc W.

APPLICANT: Retter, Marc W.

APPLICANT: Better, Marc W.

APPLICANT: Better, Johnes S.

APPLICANT: Helper W.

APPLICANT: Helper W.

APPLICANT: Helper W.

APPLICANT: Helper, William

APPLICANT: Better, William

APPLICANT: Better, William

APPLICANT: Better, William

APPLICANT: Better, William

APPLICANT: Helper, William

APPLICANT: Better, Will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 653; DB 4; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.6e-67;
Matches 128; Conservative 0; Mismatches 0; Indels
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-09-685-166A-835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
COGGANISM: Homo sapiens
US-09-636-215-835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRIGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                       61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TAASDNFQLSQGGGGGATPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                     68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GAPPLICANT:
Bangur, Chaitanya S.
APPLICANT:
Gary
Gary
APPLICANT:
Carter, Marc
APPLICANT:
Carter, Marc
APPLICANT:
CARDICANT:
COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION:
COMPOSITION:
CURRENT APPLICATION UNMERS:
CURRENT APPLICANION UNMERS:
CURRENT APPLICANION
SOFTWARE:
CURRENT APPLICANION
SEQ ID NOS:
1864
SEQ ID NOS:
1864
LENGRAND
LENGRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Score 653; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 812.7 Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Ku, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Hicham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5-09-736-457-1863
Sequence 1863, Application US/09736457
Patent No. 6509448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-09-736-457-1863
                                                                                                                                                                                                                                                                                                                                                                 121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-636-215-852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                     &
```

Length 304;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-67;
Matches 128; Conservative 0; Mismatches 0;

Henderson, Robert A. Kalos, Michael D. Fanger, Gary R. Retter, Marc W. Stolk, John A.

ö 9 63 1 TAASDNEQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV Gaps ö Length 400; Indels Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-67;
Matches 128; Conservative 0; Mismatches 0; 121 TLAEGPPA 128 128 TLAEGPPA 135 ద ò ઠે a

APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, Thomas S.
APPLICANT: Ovedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Hepler, William
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Or INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FASTSEQ for Windows Version 3.0

US-09-620-412C-349

Sequence 349. Application US/09620412C

Sequence 349. Application US/09620412C

Sequence 349. Application US/09620412C

SENERAL INFORMATION:

APPLICANT: Steven P. Fling

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DAGNOSIS OF CHLAMYDIAL INFECTION

FILE REFERENCE: 210121.469C7

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363

SOUTHARD: FRATESQ for Windows Version 3.0/4.0

SEQ ID NO 349

LENGTH: 487 GRGANISM: Chlamydia trachomatis US-09-620-412C-349 TYPE: PRT

ö

0; Gaps

Query Match
100.0%; Score 653; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels

, SEQ ID NO 852 LENGTH: 400 TYPE: PRT , ORGANISM: Homo sapiens US-09-636-215-852

121 TLAEGPPA 128 TLAEGPPA 135

1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV

ò 셤 à g ò d

0; Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 3.1e-67;
Matches 128; Conservative 0; Mismatches 0; Indels

ö

61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120 68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127 9 1 TAASDNPQLSQGGQGFALPIGQAWAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV ઠે d ò 셤

121 TLAEGPPA 128 128 TLAEGPPA 135 ð ద

US-09-685-166A

Sequence 852, Application US/09685166A

Patent No. 6630305

GENERAL INFORMATION

APPLICANT: Xu, Jiangchun

APPLICANT: Mitchan, Jennifer L.

APPLICANT: Mitchan, Jennifer L.

APPLICANT: Handever, Sousn L.

APPLICANT: Handever, Robert A.

APPLICANT: Handever, Robert A.

APPLICANT: Henderson, Robert A.

APPLICANT: Retter, Marc W.

APPLICANT: Retter, Marc W.

APPLICANT: Retter, Marc W.

APPLICANT: Garle, John A.

APPLICANT: Garle, Thomas S.

APPLICANT: Garle, John A.

APPLICANT: Heller, Darrick

APPLICANT: Wang, Aijun

APPLICANT: Hepler, William

APPLICANT: Hepler, William

APPLICANT: Hepler, William

APPLICANT: Hepler, William

APPLICANT: Retter, Darrick

APPLICANT: Beller, William

RESULT 14
US-09-598-419-349
i Sequence 349, Application US/09598419
sequence 349, Application US/09598419
sequence 349, Application US/09598419
sequence 349, Application US/09598419
set INFORMATION:
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: COMPOUNDS OF CHLAMYDIAL INPECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INPECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INPECTION
TITLE OF INVENTION: 10121.469C6
CORRENT PRILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 349
LENGTH: 487

; TYPE: PRT ; ORGANISM: Homo sapiens US-09-685-166A-852

```
Query Match 100.0%; Score 653; DB 4; Best Local Similarity 100.0%; Pred. No. 3.3e-67; Matches 128; Conservative 0; Mismatches 0;
; TYPE: PRT
; ORGANISM: Chlymadia trachomatis
US-09-598-419-333
                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               심
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VGSAPASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                        61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                 68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 TAASDNFOLSOGGOGFAIPIGOAMAIAGOIKLPTVHIGPTAFLGLGVVDNNGNGARVORV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                      1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                             8 TAASDNFÓLSÓGGGGFAIPIGOAMAIAGQÍKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 333 Application US/09598419

Patent No. 6565856

GENERAL INFORMATION:

APPLICANT: Scholler, John

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND

TITLE OF INVENTION: DATE.

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

FILE REFERENCE: 210121.469C6

CURRENT APPLICATION NUMBER: US/09/598,419

CURRENT FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 357

SOFTWARE: FactSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 333, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.464020, 412C
CURRENT APPLICATION NUMBER: US/09/620, 412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 333
                                                                                        Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 3.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indets
                                                                                                                              Indels
                                                                                 Query Match

100.0%; Score 653; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.1e-67;
Matches 128; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Chlymadia trachomatis
US-09-620-412C-333
  ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                         TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                  TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -09-620-412C-333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-598-419-333
                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \stackrel{>}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                         ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                          \dot{\delta}
```

```
61 VGSAPASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
      120
                                        68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TAASDNFQLSQGGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gabs
                                                                                                                                                                                                                                                                                                                        Sequence 196, Application US/09556877

Sequence 196, Application US/09556877

Sequence 196, Application US/09556877

GENERAL INFORMATION:
APPLICANT: Brobst, Peter
APPLICANT: Skeiky, Yasir
APPLICANT: Fling, Steve
APPLICANT: Maisonneuve, Jeff
APPLICANT: Mingons: US/09/556,877

CURRENT FILING DATE: 2000-04-19

NUMBER OF SEQ ID NOS: 305

SOFTWARE: FastSEQ for Windows Version 3.0/4.0

LENGTH: SS5

LENGTH: SS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 18
US-09-620-412C-196
Sequence 196, Application US/09620412C
Patent No. 6444234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION UNDER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 3.4e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 TLAEGPPA 135
                                                                                                                                    121 TLAEGPPA 128
                                                                                                                                                                                                 128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Chlamydia
US-09-556-877-196
```

ô

Gaps

ö

Indels

9 67

8 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV

1 TAASDNFQLSQGGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV

```
ö
                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VGSAPASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHFGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                  61 VGSAPAASLGISTGDVITAVDGAPINSATANADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                      68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                            8 TAASDNFQLSQGGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                   1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                             Gaps
                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 353, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE REPRERNET: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 653; DB 4; Length 525,
Best Local Similarity 100.0%; Pred. No. 3.4e-67;
Matches 128; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                    Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
MUMBER OF SEQ ID NOS: 357
SOFTWARE: FRAESEQ for Windows Version 3.0/4.0
                                                                                                                                                                                          0; Indels
                                                                                                                                                ; Score 653; DB 4;
; Pred. No. 3.4e-67;
0; Mismatches 0;
SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 196 LENGTH: 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 19
US-09-598-419-196
Sequence 196, Application US/09598419
Parent No. 6565856
GENERAL INFORMATION:
                                                                                                                                                    100.0%;
                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                              121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Chlamydia
US-09-598-419-196
                                                               ; TYPE: PRT
; ORGANISM: Chlamydia
US-09-620-412C-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 20
US-09-620-412C-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 196
LENGTH: 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                           ò
```

ö

ö

Length 583; Indels 60

셤

중 음

ò

Query Match
100.0%; Score 653; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.9e-67;
Matches 128; Conservative 0; Mismatches 0;

SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 353 LENGTH: 583

TYPE: PRT ORGANISM: Chlamydia trachomatis

US-09-620-412C-353

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                Sequence 353, Application US/09598419
Sequence 353, Application US/09598419
Patent No. 6565856
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: US/09/598,419
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTMARE: FREISEQ for Windows Version 3.0/4.0
SEQ ID NO 353
LENGTH: 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 337, Application US/09620412C
Sequence 337, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Score 653; DB 4; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.9e-67;
Matches 128; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 TLAEGPPA 135
                                                       128 TLAEGPPA 135
             121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 22
US-09-620-412C-337
                                                                                                                      RESULT 21
US-09-598-419-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-598-419-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                            g
ઠે
```

```
RESULT 25
US-09-598-419-309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRIGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 TAASDNEQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 67
                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TAASDNPQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                         1 TAASDNEQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                    8 TAASDNFQLSQGGGGFAIPIGGAMAIAGQIKLPTVHIGFTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                    Gaps
                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-588-419-337

US-09-588-419-337

Sequence 337, Application US/09598419

Sequence 337, Application US/09598419

Sequence 337, Application US/09598419

Sequence 337, Application US/09598419

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

CURRENT APPLICATION NUMBER: US/09/598,419

CURRENT FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 357

SOFTWARE: FastSEQ for Windows Version 3.0/4.0

LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOR TREATMENT AND INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

100.0%; Score 653; DB 4; Length 585;

Best Local Similarity 100.0%; Pred. No. 4e-67;

Matches 128; Conservative 0; Mismatches 0; Indels
                                                                                                                                           Length 585;
                                                                                                                                         Query Match

100.0%; Score 653; DB 4; Length 5.
Best Local Similarity 100.0%; Pred. No. 4e-67;
Matches 128; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 24
US-09-620-412C-309
US-09-620-412C-309
Sequence 309, Application US/09620412C
PARENT No. 6448234
GENERAL INFORMATION:
APPLICANT: Seeven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INF
FILE REFERENCE: 210121.469C7
CURRENT PELLING DATE: 2000-07-20
UNMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 337 LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-337
                                                                                  ) ORGANISM: Chlamydia trachomatis
US-09-620-412C-337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                           128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                             TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                            ò
```

```
ö
                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                               61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                 68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                        1 TAASDNFQLSQGGQGFALPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 309, Application US/09598419
Facent No. 6566856
GENERAL INFORMATION:
APPLICANT: Schely, Yasir A.W.
APPLICANT: Schely, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Mindows Version 3.0/4.0
SEQ ID NO 309
LENGTH: 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 26
US-09-620-412C-325
US-09-620-412C-325
Sequence No. 6448234
GENERAL INFORMATION:
APPLICANT: SEEVEN P. Fling
ITILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT PILING DARE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 4.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels....-
                                                                                                                                                                                              Length 619;
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                           Query Match
100.0%; Score 653; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.3e-67;
Matches 128; Conservative 0; Mismatches 0;
SOFTWARE: PastSEQ for Windows Version 3.0/4.0 SEQ ID NO 309 LENGTH: 619 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-309
                                                                                                                   , ORGANISM: Chlamydia trachomatis
US-09-620-412C-309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 TLAEGPPA 135
```

```
SEQ ID NO 317
LENGTH: 646
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 TAASDNFQLSQGGGFAIPIGGAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 325, Application US/09598419
| Sequence 325, Application US/09598419
| Patent No. 6565856
| SERERAL INFORMATION:
| APPLICANT: Scholler, John
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
| TITLE OF INVENTION: US/09/598,419
| CURRENT APPLICATION UNDERS: US/09/598,419
| CURRENT FILLING DATE: 2000-06-20
| NUMBER OF SEQ ID NOS: 357
| SEQ ID NO 325
| SEQ ID NO 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECOND STATE OF STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 653; DB 4; Length 631;
Best Local Similarity 100.0%; Pred. No. 4.4e-67;
Matches 128; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                           Length 631;
                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 4.4e-67;
Matches 128; Conservative 0; Mismatches 0;
SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ_ID_NO 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Chlamydia trachomatis US-09-598-419-325
                                                                                                                                        ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 28
US-09-620-412C-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 27
US-09-598-419-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRIGNV 127
                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                          68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                              61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TAASDNFÇLSÇGGÇGFAIPIGÇAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                 8 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                          1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 317, Application US/09598419
; Sequence 317, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Scheller, John
; TITLE OF INVENTION: DIAGNOSIS OF CHLAWYDIAL INFECTION
; TITLE OF INVENTION: DIAGNOSIS OF CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-620-412C-341

US-09-620-412C-341, Application US/09620412C

Patent No. 641, Application US/09620412C

Patent No. 641, Application US/09620412C

Patent No. 641, Application ST  

APPLICANT: Steven P. Fling

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

FILE REFERENCE: 210121 469C7

CURRENT APPLICATION UNDERS: US/09/620,412C

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Score 653; DB 4; Length (546;)
Matches 128; Conservative 0; Mismatches 0; Indels
                                                                  Length 646
                                                                                                                         Indels
                                                                    Query Match
100.0%; Score 653; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.6e-67;
Matches 128; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Chlamydia trachomatis US-09-598-419-317
) ORGANISM: Chlamydia trachomatis
US-09-620-412C-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                         121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                           128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                   ò
```

SOFTWARE: FastSEQ for Windows Version 3.0/4.0

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                           61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                              68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                 8 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TAASDNFQLSQGGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TAASDNFQLSQGGGGRAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 341, Application US/09598419
Sequence 341, Application US/09598419
Patent No. 6565856
GENERAL INPORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPROUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: LAGGE
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-66-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
LENGTH: 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 357, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT PILLING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

100.0%; Score 653; DB 4; Length 654

Best Local Similarity 100.0%; Pred. No. 4.6e-67;

Matches 128; Conservative 0; Mismatches 0; Indels
                                                                                                                                                Length 654;
                                                                                                                                                                                     0; Indels
                                                                                                                                            Query Match
100.0%; Score 653; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.6e-67;
Matches 128; Conservative 0; Mismatches 0;
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0; SEQ ID NO 341; LENGTH: 654; TYPE: PTYPE: PTYPE: PTYPE: ORGANICM: Chlamydia trachomatis US-09-620-412C-341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Chlamydia trachomatis US-09-598-419-341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                           121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 32
US-09-620-412C-357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 31
US-09-598-419-341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \stackrel{>}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                           ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                               61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TAASDNFQLSQGGQGFALPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                             68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGFRTGNV
                                                                                                                                                                                                                                                                                                                                  8 TAASDNFOLSOGGGFAIPIGOAMAIAGOIKLPTVHIGPTAFLGLGVVDNNGNGARVORV
                                                                                                                                                                                                                                                                               1 TAASDNFQLSQGGGGGAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 113, Application US/09620412C

Patent No. 6444234

GENERAL INFORMATION:

APPLICANT: Steven P. Fling

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

FILE REFERENCE: 210121.469C7

CURRENT APPLICATION NUMBER: US/09/620,412C

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 357, Application US/09598419

Sequence 357, Application US/09598419

Patent No. 656856

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, John

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DAGNOSIS OF CHLAMYDIAL INFECTION

FILE REPREBNCE: 210121.469C6

CURRENT PILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 357

SOFTWARE: FASISEQ for Windows Version 3.0/4.0
                                                                                                                                                                              Length 683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 653; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.9e-67;
Matches 128; Conservative 0; Mismatches 0;
                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 4.9e-67;
Matches 128; Conservative 0; Mismatches 0;
SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 357
LENGTH: 683
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-357
                                                                                                   ; ORGANISM: Chlamydia trachomatis
US-09-620-412C-357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 34
US-09-620-412C-313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 33
US-09-598-419-357
```

ö

```
61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                        8 TAASDNFQLSQGGGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 67
                                                                                                                                                                                                                                                                                                              1 TAASDNFQLSQGGQGFAIFIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                           ó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-00-598-419-313

Sequence 313, Application US/09598419

Patent No. 656356

GENERAL INFORMATION:

APPLICANT: SKELKY, Yasir A.W.

APPLICANT: SCHOLIE: John

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

FILE REFERENCE: 210121.46.8C6

CURRENT APPLICATION NUMBER: US/09/598,419

CURRENT FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 357

SOFTWARE: FastSEQ for Windows Version 3.0/4.0

SEQ ID NO 313

LENGTH: 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 345, Application US/09620412C
Sequence 345, Application US/09620412C
Seatent No. 644824
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
                                                                                                                                                                                           Query Match

100.0%; Score 653; DB 4; Length 691;
Best Local Similarity 100.0%; Pred. No. 5e-67;
Matches 128; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 653; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5e-67;
Matches 128; Conservative 0; Mismatches 0; Indele
SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 313 LENGTH: 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Chlamydia trachomatis
                                                                                                            ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-620-412C-345
                                                                                                                                        US-09-620-412C-313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-598-419-313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                 엄
                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWOTKSGGTRTGNV 120
                                                                                                                                                                                                               61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                          68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                      1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 60
                                                                                                                                                      8 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGFTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 345, Application US/09598419
Patent No. 656886
GENERAL INPORMATION:
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION TITLE REFERENCE: 210121.469C6
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE; FREISEQ FOR Windows Version 3.0/4.0
SEQ ID NO 345
LENGTH: 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/09620412C
Sequence 321, Application US/09620412C
Patent No. 64464234
GENERAL INFORMATION:
TRIBLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DAIRS: 2000-07-20
NUMBER OF SEQ ID NOS: 363
  Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 5.1e-67;
Matches 128; Conservative 0; Mismatches 0; Indels
                                                   0; Indels
100.0%; Score 653; DB 4;
100.0%; Pred. No. 5.1e-67;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Chlamydia trachomatis US-09-598-419-345
  Query Match
Best Local Similarity 100.
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                      121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                   128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 38
US-09-620-412C-321
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 37
US-09-598-419-345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
```

SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 345 LENGTH: 700

; TYPE: PRT ; ORGANISM: Chlamydia trachomatis US-09-620-412C-345

```
0
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                  68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                         61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPIVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                             1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                           8 TAASDNPOLSOGGOGFAIPIGOAMAIAGOIKLPTVHIGPTAFLGLGVVDNNGNGARVORV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TAASDNFQLSQGGGAAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 653; DB 4; Length 715;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                  Length 715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 321, Application US/09598419
Patent No. 6565856
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Skely, Yasir A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSTS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT PELLING ATTE: 2000-66-20
NUMBER OF SEQ ID NOS: 357
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATI
TITLE OF INVENTION: COMPOSITIONS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
LENGTH: 715
                                                                                                                                                               Query Match

100.0%; Score 653; DB 4;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 128; Conservative 0; Mismatches 0;
SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 321
LENGTH: 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 329, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-329
                                                                       ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-620-412C-329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -09-598-419-321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                         ò
```

```
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 TAASDNFOLSOGGGFAIPIGOAMAIAGOIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                       Sequence 129, Application US/09598419
Patent No. 656586
GENERAL INPORMATION:
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION MESSER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FRACES for Windows Version 3.0/4.0
SEQ ID NO 329
LENGTH: 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 653; DB 4; Length 715;
100.0%; Pred, No. 5.3e-67;
iive 0; Mismatches 0; Indele (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cch completed: April 20, 2004, 06:25:00 time : 23 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
  121 TLAEGPPA 128
                                          128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TLAEGPPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 TLAEGPPA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 128; Conserv
                                                                                                                                  US-09-598-419-329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search
Job tim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

ö

ö

Length 715; Indels

Query Match
100.0%; Score 653; DB 4;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 128; Conservative 0; Mismatches 0;

SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 321 LENGTH: 715

TYPE: PRT; ORGANISM: Chlamydia trachomatis US-09-598-419-321

67

음

ò

g

8

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

nucleic search, using frame plus p2n model

OM protein -

```
Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1h
-MODEL=frame+ p2n.model -DEV=x1h
-MODEL=frame+ p2n.model -DEV=x1h
-DEV=xnl
-DEV=
April 29, 2004, 20:32:52; Search time 3784.74 Seconds (without alignments) 1511.672 Million cell updates/sec
                                                                                                                                                                                               675
1 TAASDNFQLSQGGQGFAIPI.....QTKSGGTRTGNVTLAEGPPA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3470272 segs, 21671516995 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                           7.00
                                                                                                                                                                                                                                                                                                BLOSUM62
Xgapop 10.0 , Xgapext 0
Ygapop 10.0 , Ygapext 0
Fgapop 6.0 , Fgapext 7
Delop 6.0 , Delext 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                            US-09-684-215B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_ro:*
em_sts:*
em_un:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  em_pat:*
em_ph:*
em_pl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_om:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  em_ov:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenEmbl:*
                                                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
               Run on:
```

```
30: em htg hum:*
31: em htg luw:*
32: em htg luw:*
33: em htg mus:*
34: em htg mus:*
35: em htg mus:*
36: em htg vd:*
37: em htg vd:*
38: em htg vd:*
40: em htgo mus:*
40: em htgo mus:*
41: em htgo mus:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ш
н
œ
4
Σ
Σ
₽
ശ

Result		Query	1000	0	ç	To so the state of	
I I I	2000	March 1	11191191	9 !		1 :	-
·H	67	00	7			51334 Fused	pro
8	~	00.	0		0374	03747 S	Ö
m	~	00	9		7403	74032 8	ces
4	\sim	100.0	w		8	5788 5	
ស	~	00	14		7403	1033 S	cea
9	^	8	7		00579	90 Sequen	
7	~	8	8		25132	1322 Fused	pro
80	^	00	8		30312	3127	e O
6	^	00	228		0373	3735	oe Oe
10	7	00	1402	Н	06925	06925	41
11	~	8	9		3425	1257	acte
12	7	00	4305		833	34	cte
13	~	Ψ.	44		5915	9152	9
14	7	ď.	₹"		4	142	c e
15	~	œ.	4,		2	325	9
16	~	φ.	4		9	97	e e
17	~	Ψ.	4		2	302	9
18	~	ď	4		9	969	Ge Ge
19	^	φ.	4.		8	581	Ö.
20	~	ω.	4,		332	325	nds
21	^	œ.	4		4	145	nds
22	7	6.	4		5928	82	nds
23	7	φ.			381	317	nds
24	^	ė.			5916	165	90
25	7	φ.			3245	52	90
26	~	œ.	1872		9483	AR194838 Sequence	Ge Ge
27	^	ο.			3311	120	ge Ge
28	\sim	φ.			5331	315	o e
29	\sim	œ.			2960	209	o e
30	_	φ.			259	2594	oe O
31	~	o,			9633	338	nds
32	\sim	o,			645	06458	nds
33	\sim	a,			5929	59298	nds
34	~	o,			83	05830	nds
35	ന	е Э	675		5127	51272 S	çe
36	ന	ë.	675		0053	0535 8	e S
37	ന	ო	675		0280	35802 S	Ce
38	ന	e.	675		1104	1049 S	ce
39	ന	<u>.</u>	675		784	57848 S	o O
40	ന	93.6	822		7764	77645 S	o O
41	ന	ω.	822		5915	59152 Sequ	e c
42	ന	93.6	894		5148	51489 Se	e Ce
43	632	93.6	900	9	\sim	0690 Sednen	e C
44	ന	93.6	900		36296	65960 Se	Çe
45	m	93.6	915		128	61281 S	ce

0)

ALIGNMENTS

RESULT 1

```
and
                                                                                                                                                    ... and Neto,A.C.

2002510494-A 13 09-APR-2002;

Artificial Sequence
PN JP 2002510494-A,13
PD 09-APR-2002
PP 07-APR-1999 JP 200542460
PR 07-APR-1999 JP 2005555,30-DEC-1998 US 09/223040 PI
ASIR A W SERIKY, MARK ALDERSON, ANTONIO CAMPOS NETO PC
C12N15/09, AGIK39/04,AGIK48/00,AGIP31/04,CO7K14/35,CO7K19/00, PC
C12N15/09, AGIK39/04,AGIK48/00,AGIP31/04,CO7K14/35,CO7K19/00, PC
C12N21/02, C12N15/00
CC Description of Artificial Sequence:bi-fusion
procein Ral2-DPPD
CC heraing frame 1
CC Di-fusion protein Ral2-DPPD (dc-
CC reading frame 2
PH Key
FT CDS
FT CDS
FT CDS
                                                                                                      BD251334
BD251334.1 GI:33061104
BD251334.1 GI:33061104
BD251334.1 GI:33061104
Synthetic construct
synthetic construct
synthetic construct
synthetic construct
synthetic construct
artificial sequences.
I (bases 1 to 702)
Skeiky,Y.A.W., Alderson,M. and Neto,A.C.
Skeiky,Y.A.W., Alderson,M. and Neto,A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mtb24), reading frame 1
bi-fusion protein Ral2-DPPD (designated Mtb24),reading frame 1
reading frame 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 IleThralaValaspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                   BD251334 702-2003 Fused protein of Mycobacterium tuberculosis antigen and utilization thereof.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     707
1132
000
000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Conservative:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215B-4 (1-132) x BD251334 (1-702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.376-42
675.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
Score:
Fercent Similarity:
Dest Local Similarity:
Ucbery Match:
Fercent Similarity:
Fercent Simil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
SOURCE
BD251334
LOCUS
DEFINITION
                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Бb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 B 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

Db 1030 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 1065	RESULT 4 AX005788 AX005788 LOCUS LOCUS DEFINITION Sequence 907 from Patent W09909186. ACCESSION AX005788 VERSION AX005788 ACCESSION AX005788 VERSION AX005788	XEYWOKUS Aycobacterium tuberculosis SOURCE Mycobacterium tuberculosis ORGANISM Mycobacterium tuberculosis Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales; Corynabacterinaes; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.	REFERENCE 1 AUTHORS Portnoi,D. and Guigueno,A. TITLE Polypeptide nucleic sequences exported from mycobacteria, vectors TITLE Comprising same and uses for diagnosing and preventing tuberculosis JOURNAL PATENT: WO 9909186-A 907 25-FEB-1999; PORTNOI DENIS (FR); GUIGUENO AGNES (FR)	FEATURES Location/Qualifiers Source 1.068 /organism="Mycobacterium tuberculosis" /mol_type="unassigned DNA" /db xref="taxon:1773"		/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xxef="REMTREMEN:CACOSION">/db.xx	NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHYGDVISVI WQTKSGGTRTGNVTLAEGPPA" ORIGIN	: 3.59e-42 675.00 cy: 100.00%	Mismatches: Indels: Gaps:			Oy 21 GlyGlnalaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40	QY 41 IleGlyProThrAlaPheLeuGlyVeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60	Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAepVal 80	Qy 81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100	Qy 101 GlyHisHisProGlyAspValileSerValThrItpGlnThrLysSerGlyGlyThrArg 120
ACCESSION BD274032 VPRSTON BD274032.1 GT:33083800	-	REFERENCE 1 (bases 1 to 1068) AUTHORS dicquel, B., Pertnoi, D., Lim, E., Pelicic, V., Guigueno, A. and Salmoniere, Y.G.D.L. TITLE Sequences nuclieic acid from polypeptides exportes from mycobacteries, vector the comprenant and applications at diagnostic	JOURNAL PATENTY PASTERS 22-0CT-2002; COMMENT OS Mycobacterium tuberculosis PN JP 2002534956-A/256 PD 24-0CT-2002	PR 14-AUG-1997 FR 97/10404,11-SEP-1997 FR 97/11325 PI BRIGITTE GTCQUEL, DENIS PORTNOI, ENG-MONG LIM, VLADIMIR PELICIC, PI BANES GUIGUENO, YVES GOGUET DE LA SALMONIERE PC C12N1S/09, AGIKS9/04, AGIK48/00, AGIR1/100, AGIP31/04, CO7K14/35, PC C07K16/12,	PC (CMX19/00,Cl2N1/21,Cl2M21/04,Cl2N1/02,Ll2N1/08,CULN33/59, FC GQ1N33/53// (Cl2N15/00,(Cl2N15/00,(Cl2N15)20, FC	80 14	Length: Matches:	nilarity: 100.00% Similarity: 100.00% h: 6	US-09-684-215B-4 (1-132) x BD274032 (1-1068)	67	Qy 21 GlyGlnblaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40	Qy 41 IleglyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAsnGlyAlaArg 60 	Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80	81 IleThralaValaspGlyalaProlleAsnSerAlaThrAlaMetAlaAspAla 910 ArraccescenceAccescenceAstraCoccatceGocaTGGCGGACGC	101 GlyHisHisBroGlyAspValIleSerValT	121

ò g g / S

q

ર્જ

ઠે

g ઠે

Portnol, D., and cullqueno, A.

Polypeptide nucleic sequences exported from mycobacteria, vectors comprising same and uses for diagnosing and preventing tuberculosis comprising same and uses for diagnosing and preventing tuberculosis patent; WO 9909186-A 909 25-FEB-1999;

Patent: WO 9909186-A 909 25-FEB-1999;

Portnoi Denis (FR); GuidGueNo AGNES (FR)

Location/Qualifiers

1. 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1144

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| . 1143

| 1044 PAT 24-AUG-2000 804 40 9 100 Mycobacterium tuberculosis Mycobacterium tuberculosis Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterinaes, Mycobacteriaceae, Mycobacterium, Mycobacterium tuberculosis complex. 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlnGlyPheAlaileProile 925 GTCCAACGCGTGGGTCGGGGAGCGCTCCGGCAAGTCTCCGCATCTCCACCGGCGACGTG

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                           g
                                                         à
                                                                                 셤
                                                                                                                 ઠે
                                                                                                                                            d
                                                                                                                                                                    ठे
                                                                                                                                                                                                    ď
                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C12NIS/00
Description of Artificial Sequence:tri-fusion protein Ral2- CC
TBHS-RA35
(designated Mtb32A)

n = g, a, c or t

n = g, a, c or t

n = g, a, c or t

Rey
Therefore the cor t

Rey
                                                                                                                                                                                                                                                                                                                                                       BD251322.1 GI:33061092
JP 2002110494-A/1.
synthetic construct
synthetic construct
synthetic sonstruct
artificial sequences.
1 (bases 1 to 2287)
Skeiky, Y.A.W., Alderson, M. and Neto, A.C.
Elvsed protein of Mycobacterium tuberculosis antigen and utilization
thereof
                                                                                                                                                                                                                                                                                                 BDS51322 2287 bp DNA linear PAT 17-JUL-2003
Fused protein of Mycobacterium tuberculosis antigen and utilization
thereof.
                                                                                                                               985 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACGCGGATGGCGGACGCGCTTAAC 1044
                                                                                                                                                                              1045 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGT 1104
                                                                                                                                                          101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                    81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
925 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 984
                                            61 ValGinArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF 07-APR-1999 JP 2000542460
PR 07-APR-1999 US 09/223040 PI 98.05 O9/223040 PI 98.05 O9/223040 PI 98.05 O9/05056,30-DEC-1998 US 09/223040 PI YASIR A W SKEIKY, MARK ALDERSON, ANYONIO CAMPOS NETO PC C12N15/09, A61K39/04, A61K48/00, A61P31/04, C07K14/35, C07K19/00, PC C12N15/09
CC Describtion of
                                                                                                                                                                                                                                     1105 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 1140
                                                                                                                                                                                                                      121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent: JP 2002510494-A 1 09-APR-2002;
CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (42). .(2231)
diffed base (2270).
Location/Qualifiers
1...2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-4 (1-132) x BD251322 (1-2287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Artificial Sequence
JP 2002510494-A/1
09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.67e-42
675.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified_base
CDS
modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSSSEEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .. No. .
                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                             BD251322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                           à
                                                                      ద
                                                                                                    à
                                                                                                                               셤
                                                                                                                                                              ઠે
                                                                                                                                                                                      g
                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                               g
```

```
linear PAT 12-JUN-2003
                                          242
                                                                                                                          243 erccaacecereerceeaacecrcceeceaaacacarcrccacarcrccacarcrccaceacere 302
                                                                                                                                                                       81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                 303 ATCACCGGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 362
                                                                                                                                                                                                                                                          101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                        363 GGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGCGGCACGCGT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCACGACGCACGA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
60
                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GlyGlnAlaMetAlaileAlaGlyGlnileArgSerGlyGlyGlyGerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 2287)
Skeiky, Y., Alderson, M. and Campos-Neto, A.
Fusion proteins of mycobacterium tuberculosis antigens and their
                                          183 Arcececracecerrecreseerreserreseeraseaeaacaacsaceaacea
                                                                                  61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                               121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                         423 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: US 6544522-A 1 08-APR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2287 bp
Sequence 1 from patent US 6544522.
AR303127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-4 (1-132) x AR303127 (1-2287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .2287
/organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR303127.1 GI:31691855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.67e-42
675.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
AR303127
```

63 AGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGGCAGGATTCGCCATTCCGATC 122

1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProlle 20

21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis

```
RESULT 10
AE006925
LOCUS
DEFINITION
                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                          JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                         Unknown.
Unclassified.
Unclassified.
1 (2287)
Reed,S.G., Skeiky,Y.A., Dillon,D.C., Alderson,M. and Campos-Neto,A.
Fusion proteins of Mycobacterium tuberculosis antigens and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 GICCAACGCGGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCACGGCAACGTG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 ileThralaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT 18-DEC-2003
                                                          GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ValGlnhrgValValGlySerhlaProAlaAestreuGlyIleSerThrGlyAspVal 80
                   363 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCACGCGT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 302
                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                              2287
132
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                             ACAGGAACGTGACATTGGCCGAGGGACCCCCGGGCC 458
                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                               Patent: US 6627198-A 1 30-SEP-2003;
Location/Qualifiers
1.2287
/ Organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                            AR403735 2287 bp
Sequence 1 from patent US 6627198.
AR403735 GI:40151411
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-4 (1-132) x AR403735 (1-2287)
                                                                                                                                                                                                                                                                                                                                                              7.67e-42
675.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                             .
Unknown.
                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
    243
                                                                                                                       423
                                                              101
                                                                                                                                        RESULT 9
AR403735
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
KEYWORDS
SOUNCE
ORGANISM
                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     원 상
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
    8 8
                                      셤
                                                        \delta
                                                                             ద
                                                                                              · &
                                                                                                                    셤
```

```
Missocretium tuberculosis CDC1551

Mycobacterium Mycobacteriaces; Mycobacterium, Mycobacterium CDCyrpebacterium tuberculosis compile.

The Reses 1 to 14029

Mycobacterium, Mycobacterium tuberculosis clinical and laboratory Strains.

Mycolagenome comparison of Mycobacterium tuberculosis clinical and laboratory strains

Mycobacterium tuberculosis clinical and laboratory mycobacterium tuberculosis CDC1551"

My
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MIVUI30"

complement (643. .1062)
/gene="MIVUI30"
/gene="MIVUI30"
/note="identified by Glimmer2; putative"
/codon start=1
/codon start=1
/product="Mypothetical protein"
/protein_id="AAK44354.1"
/protein_id="AAK44354.1"
/protein_id="MAK4358.1LRHCVSDDQVTVVGFDGDDLGKTARRIAALVVQRA
/translation="MASSSSIPLIAHCVSDDQVTVVGFDGDDLGKTARRIAALVVQRA
IFLNDRNTAVAHSGDDAVLGHAVLPGVPRDPDPLHASSMYSILGMCQSVNGRPFDAIA
LVSVRLCTVQTDPTDSCGGRDRPGQLPCAPLDYHRHH"
AB006925
Mycobacterium tuberculosis CDC1551, section 11 of 280 of the complete gamome.
AB006925 AB000516
AE006925.1 GI:13879610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1047. .1415

/gene="MT0131"

1047. .1415

/gene="MT0131"

/note="identified by match to protein family

/codon start=1

/rans1 table=11

/product="DNA-binding protein, CopG family"

/protein_id="AAK44355.1"
```

```
/producE="serine protease, putative"
/producE="serine protease, putative"
/protein_id="Ap&44357.1"
/brotein_id="Ap&44357.1"
/brotein_id="MSNSRRRSILRWSWILLSVILAAVGIGIATAPAQAAPPALSQDRFAD
FAPLPIDPSAMYAQVGPVVNINTKTGASTGTGIVIDPNGVVLTNINTVAGATD
INAFSVGSGGTYGAVVGYDRTODVAVLQLEAGAGTGIPSAAIGGGVAVGESVVAMGNSG
GQGGTPRAVPGRVVALGQTVQASDSLTGAEETLAGLIQPDAAIQPGDSGGPVVNGLGQ
NVGMNTRASDRPQLSGGGGFAIPIGQAMAIAQQIRSGGGSPTVHIGPTAFLGLGVVD
NNGNGBRVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVT
MQTKSGGTRTGNVTLABGPPA"
                                                                                                                                                                                                                                                                                                                                                                                          araa pittavtaagadevsaalaalesghaqavqalsaqaaaafhoopvotlaggagagaya
aaeaqveqollaainaptqallgrpligngadgapgtgqaggaggaggilygnggygg
agqaggaggpaglighgggggaggggaaggagaggggggggggagyg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHGGAGGAAGGAGGGGGGGGGGGGGGABANIVSGGDGGLGGAGGGGGGGGWIYGDGGAGGGGG
QGAGGGAGGAGGDGGQGGAGGLWGTGGAAGGHGGQGGGTGGPPLPGQAGWGAAGGAGG
LIGNGGAGGDGGVGASGGGVAGVXGAGGNAMLIGHGGAAGGAGGDSSPANGAAGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHLFGNGGSGCHGGAVTAGNTGIGGAGGVGGDARLICHGGAGGAGGDRAGALVGRDGG
PGGNGCAGGQLYGNGGDGGPGGQGGQAFGANNIGGTGGAGGNGGPAILSGNGGNGGAG
GAGGAGGAGGAGGVGGAGGAPGTGGTLQAAVSGLVTALFGAPGQPGDTGQPG"
                     /tränslation="mykkprnpadyvigddvevsdvdlkogevyvdgerlyderveom
asesirlarereanlipggkslsggsahspavqvvvskathaklkelarsrkmsvsk
                                                                                                                                                                                                                                                                                                                                                                       translation="MFAGGGAGGLGRCVMSFVSVAPEIVVAAATDLAGIGSAISAANA
                                                                                                                                                                                              note="similar to GB:AL123456; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to GP:2808807; identified by sequence similarity putative" /codon_start=1 /trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="similar to GP:2808801; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3519. .4586
//gene="MT0133"
3519. .4586
//gene="MT0133"
//note="identified by match to protein family HMM"
/codon start=1
/transl_table=11
                                                                                                                                                                                                                                                                    /transI_table=11
/product="PE PGRS family protein"
/protein.id="AAK44356.1"
/db_xref="G1:13879614"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/product="pep2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity, putative"
/codon_start=1
/transl_table=11
'db_xref="GI:13879613"
                                                                                                                                                                                                                   similarity; putative"
/codon start = 1
/transI table = 11
                                                                   LRPVLDEFVQRETGRILPRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4695. .6500
/gene="MT0134"
4695. .6500
/gene="MT0134"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="MT0135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6603. .7970
/gene="MT0135"
                                                                                             1682. .3367
/gene="MT0132"
                                                                                                                                                .682. .3367
'gene="MT0132"
```

gene

CDS

gene

gene

CDS

```
/product=hypothetical protein"
/product=hypothetical protein"
/product=hypothetical protein"
/protein id="AAK44560.1"
/brotein id="AAK44560.1"
/brotein id="AAK44560.1"
/brotein id="AAK44560.1"
/brotein id="AAK44560.1"
/translation="WORENYDEALSWULAALAGILGATAFTHSAGYFVTFWTGNSO
RAVIGLEGDDAWMSVTASLILIEFVAGVVIASVCRRHFWAAHPHGBTVLTTFSLIFAA
RAUAGGKVEDMLGYFLIHASFVLGAAAGGAISMYTGPQMLAVAAVVCAATTGYTKH
ADRRGLINNQKRAQGGKKLFRALKRGELDSGTSTPATNYGSS"
complement (8949. .9989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fransī table=11
/product==esterass, putative, antigen 85-C"
/product==esterass, putative, antigen 85-C"
/product==seterass, putative, antigen 85-C"
/brocein_id="ARK44361.1"
/db_xref="d1:13879619."
/db_xref="d1:13879619"
/db_xref=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4188 AcedecedercearaAcrifecaecrereceaegeeeeeeeaearifeecarreceare 4247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 GlyGlnalaMetAlaileAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyBheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to SP:P08634 PID:46222; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to SP:P31953 GB:X57229 PID:48828
PID:1567734 PID:1877254; identified by sequence
similarity; putative"
/codon.start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/ransi_table=1
/product="nodulation protein N-related protein"
/protein_id="AAK44362.1"
/db_xref="G1:13879620"
                                8038. .8817
/gene="MT0136"
/gene="MT0136"
/gene="MT0136"
/note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-4 (1-132) x AE006925 (1-14029)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (8949. .9989)
/gene="MT0137"
                                                                                                                                                                                                                                                                                                  table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .0218. .10673
/gene="MT0138"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="MT0138"
                                                                                                                                                                                                                                                    /codon_start=1/transl_table=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="MT0137"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atppaapaapa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.66e-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     675.00
100.00%
100.00%
RLTAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

LLGLIVSSAVCGTGTGEVTFTREPDVELPFAAQPRVCDAEQSNTSVIFDRRALLKVFR RVSSGINPDIELNRVLTRAGNPHVARLLGAYQFGRPNRSPTDALAYALGMVTEYEANA AEGWAMATASVRDLPAEGDLYAHEVGGDFAGESYRLGBAVASVHATLADSLGTAQATF

gene

CDS

/protein_id="AaK44359.1" /db_xref="G1:13879617" /translation="MTKSDTLATKLPWSDMLPRQRWYAGRNRELATVKPGVVVALRHN LDLVLVDVTYTDGATERYQVLJVGWDFBPASBYGTKAALGVADDRTGFDALYDVAGPQF PUDRULARIJSTVAVVPELREYAPTIEQQPOKLAAEAITVQRVHGDIHLGQVLRTPES WILI IDPEGEPGQPLDERRAPDSPLRDVAGVIRSFEYAAYGPLVDQATDKQLAARAREW VERNRAAFCDGYAVASGIDPRDSALLIGAYELDKAVYETGYETRHRPGWLPIPIRSIA

```
.
.
.
.
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBMED; 12368430.
Camus J.C., Pryor M.J., Medigue C., Cole S.T.;
"Re-annocation of the genome sequence of Mycobacterium tuberculosis H37Rv";
Microbiology 148:2967-2973(2002).
                                                                                                                                                                                                                                                                                                                                                                                                   BX842572; ALO21427; ALO21428; ALO21926; ALO21927; ALO21928; ALO21929;
ALO21930; AL123456; Z74410; Z80233; Z80775; Z86089; Z92669; Z92770; Z96071;
Z97050;
                                                                                                                                                                                                                                                      4547
                                                             4367
                                                                                                                          4427
                                                                                                                                                                             DUBMED, 9634230.

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry III C.E., Tekaia F., Badcock K., Basham D., Srown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Murphy L., Oliver S., Goborne J., Guail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.B., Taylor K., Whitchead S., Barrell B.G "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence".
                                                                                                                                                                                                                        120
81 IleThralavalaspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-JUN-1998) to the EMBL/GenBank/DDBJ databases. Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams. Sanger Centre, Wellcome Trust Genome Campus, Hinxton. Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail:
                            9
                                                                                           80
                                                    1368 GTCCAACGCGTGGGCGAGGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGAGCGTG
                                                                                                                                                                                                                                         ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                        GlyHisHisProGlyAspValileSerValThrTrpGlnThrLy8SerGlyGlyThrArg
                                11eGlyProThrAlaPheLeuGlyLeuGlyValValAspAspAspAspGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex; Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis H37Rv complete genome; segment 1/13
                                                                                                                                                                                                                                                                                                                                                                                 standard; circular genomic DNA; PRO; 341957 BP.
                                                                                                                                                                                                                                                                                                              ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 4583
                                                                                                                                                                                                                                                                                     ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-2003 (Rel. 77, Created)
21-NOV-2003 (Rel. 77, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
MEDLINE; 98295987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkhill J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX842572.1
                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                       4548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-341957
     1248
                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                       BX842572
                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                      셤
                                   ò
                                                         g
                                                                                             8 8
                                                                                                                                                   ∂
                                                                                                                                                                                                                           ò
```

```
parkhill@sanger.ac.uk
```

/note="Ravool, (MT001, MTV029.01, P49993), len: 507 aa. dnaA, chromosomal replication initiator protein (see citations below), equivalent to other Wycobacterial CHROMOSOMAL REPLICATION INITIATOR PROTEINS e.g. p46388 DNAA WYCDA from Wycobacterium leprae (502 aa); P46388 DNAA WYCDA from Wycobacterium paratubearculoais (509 aa); P49992 DNAA WYCDA from Mycobacterium smegmatis (504 aa); P49992 DNAA WYCDA from Mycobacterium smegmatis (504 aa); P49992 DNAA WYCDA from Wycobacterium smegmatis (504 aa); P49992 DNAA WYCDA from Wycobacterium smegmatis (504 aa); P49992 DNAA WYCDA from Wycobacterium smegmatis (504 aa); P49992 DNAA STRCH CHROMOSOMAL REPLICATION INITIATOR PROTEIN from Streptomyces reticuli (643 aa); DSAA ECOLI F03004 B3702 chromosomal replication initiator protein from Escherichia coli strain K12 (467 aa); PASTA scores opt: 986, E(): 0, (43.24 identity in 389 aa overlap); etc. Contains PS00017 ATP/GTP-binding site motif A (P-loop) and PS01008 DnaA protein signature. BELONGS TO THE DNAA PAMILY. Note that the first base of this gene has been taken as base 1 of the Mycobacterium tuberculosis H37RV genomic sequence." /mol_type="genomic DNA" /organism="Mycobacterium tuberculosis H37Rv" /strain="H37Rv" Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) /db xref="taxon:83332" /mol type="genchical /evidence=EXPERIMENTAL Location/Qualifiers source CDS Sey

// function="PLAYS AN IMPORTANT ROLE IN THE INITIATION AND // function="PLAYS AN IMPORTANT ROLE IN THE INDS TO THE ORIGIN OF REDUICATION, IT BINDS SPECIFICALLY DOUBLE-STRANDED DNA AT A B BR CONSENSUS (BNAA BOX): 5'-TATAC(C/A) A (C/A) A (2') A 13'-DINDS TO ATP AND TO ACIDIC PHOSPHOLIPIDS. DNAA PROTEIN BINDS THE ORIGIN OF REPLICATION (OriC), ATP AND ADP, AND EXHIBITED WEAK ATPASE ACTIVITY." ′gene≂"dnaA"

THE TOTAL TOTAL STATES OF THE TOTAL STATES OF TOTAL STATES OF THE TOTAL STATES OF TOTAL STATES OF THE TOTA /Jocus_tag="Rv0001" /product="CHROMOSOWAL REPLICATION INITIATOR PROTEIN DNAA" /protein id="CAA16238.1" /franslation="MYDDPGSGFTTVWNAVVSELNGDPRVDGPSSDANLSAPLTPQQR

Cost. :252 (MTCY1014.0), len: 402 aa. dnaN, Incre="Rv0002, (MTV029.02, MTCY1014.0), len: 402 aa. dnaN, Incre="Rv0002, (MTV029.02, MTCY1014.0), lee citations DNA polymerase III (beta chain) (EC 2.7.7.7) (see citations below), equivalent to other Mycobacterial DNA POLYMERASES III BETA CHAIN e.g. NP 301130.1|NC 0026/7 from Mycobacterium leprae (399 aa); 991716|DP3B MYCPA from Mycobacterium subap. paratuberculosis (399 aa); P52851|DP3B MYCPA from Mycobacterium snegmatis (399 aa); P52851|DP3B MYCPA from Mycobacterium snegmatis (399 aa); P52851|DP3B MYCPA from Mycobacterium snegmatis (399 aa); B7381|IBSTA CHAIN from Streptomyces coelicolor (376 aa), FASTA scores: opt: 1189; E(): 0, (52.8% identity 1384, 1440 /note="PS01008 DnaA protein signature" misc_feature misc_feature

SOS

```
avium subsp. paratuberculosis (166 aa); and highly similar to NP 301132.1|NC 002677 conserved hypothetical protein trom Mycobacterium leprae (189 aa); 570990 hypothetical protein from Mycobacterium smegmatis (194 aa). Also highly similar, except in N-terminal part, to
                                                                                                                                                                                                                                            1.12e-39
675.00
100.00$
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hewinson, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Garnier, 7
                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                               Best Local S
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
REMARK
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX248334
   FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene_rec_
/yeace_rec_
/yeace_rec_
/product="nan Replication and Repair Protein RecF
/product="nan Replication"
/protein_id="CABO242.1"
/protein_id="CABO242.1"
/brotein_id="CABO242.1"
/brotein_id="CABO242.1"
/brotein_id="CABO242.1"
/brotein_id="CABO242.1"
/brotein_id="CABO242.1"
/brotein_id="CABO242.1"
/brotein_id="CABO242.1"
/brotein_id="CABO242.1"
/brotein_id="CABO242.1"
/brote="Protein RecF | Protein Repair RecF | Protein Repair Repair RecF | Protein Repair Repair RecF | Protein Repair Repair Repair Repair RecF | Protein Repair RecF | Protein Repair Repair Repair Repair Repair Repair Repair RecF | Protein Repair Repair Repair Repair Repair RecF | Protein Repair Repair Repair Repair Repair RecF | Protein Repair Repair RecF | Protein Repair RecF | Protein RecF | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=EXPERIMENTAL
/note==RX0003, (MTCY10H4.01), len: 385 aa. recF, DNA
replication and repair protein (see citations below),
equivalent to others Mycobacterial DNA replication and
repair proteins e.g. NP 30131.1 |NC 002677 from
Mycobacterium leprae (385 aa); O9L715/RECF MYCPA from
Mycobacterium avium subsp. paratuberculosis (385 aa);
PSO916/RECF MYCSM from Mycobacterium smegmatis (384 aa);
etc. Also hīghly similar to others e.g. P36176/RECF STRCO
DNA REPLICATION ND REPAIR PROTEIN from Streptomyces
coelicolor (373 aa); NP 440892.1 |NC 000911 from
Synechocystis sp. strain PCC 6803 (384 aa);
NP 469352.1 |NC 000312 from Listeria innocus (370 aa); etc.
Contains PS00017 ATP/GTP-binding site motif A (P-loop),
PS000617 RecF protein signature 1, and PS00618 RecF protein
signature 2. BELONGS TO THE RECF FAMILY."
                                                                                                                                                                        /EC_number="2.7.7.7"

/Function="DNA POLYMERASE III IS A COMPLEX, MULTICHAIN
Function="DNA POLYMERASE III IS A COMPLEX, MULTICHAIN
ENCYME RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN
ENCYMEASE ACTIVITY. THE BETA CHAIN IS RESOURED FOR
INITIATION OF REPLICATION ONCE IT IS CLAMPED ONTO DNA, IT
SLIDES FREELY (BIDIRECTIONAL AND ATP-INDEPENDENT) ALONG
DUDLEX DNA (CATALITIC ACTIVITY: N deoxynucleoside
LTIPDASPHATE = N diphosphate + {DNA}N]."
//cous_tag="RAGOOG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="THE RECF PROTEIN IS INVOLVED IN DNA METABOLISM AND RECOMBINATION; IT IS REQUIRED FOR DNA REPLICATION AND NORMAL SOS INDUCIBILITY. RECF BINDS PREFERENTIALLY TO SINGLE-STRANDED, LINEAR DNA, IT ALSO SEEMS TO BIND ATP."
   in 337 aa overlap); P21174 | DP3B MICLU from Micrococcus luteus (310 aal); P52023 | DP3B SYNP7 from Synechococcus sp. strain PCC 7942 (375 aa); etc. Overlaps and extends CDS ineighbouring cosmid MTCX10H4.01."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=EXPERIMENTAL
/note="Rv0004, (MTCY10H4.02), len: 187 aa. Conserved
/nyochetical protein (see Salazar et al., 1996), highly
similar, but longer 21 aa in N-terminus, to
AAF33696.1|AF222789 unknown protein from Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="DNA POLYMERASE III (BETA CHAIN) DNAN (DNA NUCLEOTIDYLTRANSFERASE)" /protein id="CAA16239.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4243. .4296
/note="PS00618 RecF protein signature 2"
4434. .4997
                                                                                                                                                 transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="recF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
```

```
151817 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGTGGGGCAGGGATTCGCCATTCCGATC 151876
                                                                                                                                                                                                                                                                                                                                                                                                                                                         151997 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 152056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BX248334 11-JUN-2003 AX248334 Script 11-JUN-2003 Mycobacterium bovis subsp. bovis AF2122/97 complete genome; segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garnier,T., Biglmeier,K., Camus,J.-C., Medina,N., Mansoor,H.,
yryor,M., Duthoy,S., Grondin,S., Lacroix,C., Monsempe,C., Simon,S.,
Harris,B., Atkin,R., Doggett,J., Mayes,R., Keating,L.,
Wheeler,P.R., Parkhill,J., Barrell,B.G., Cole,S.T., Gordon,S.V. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire Sacterienne Institut Pasteur 28,rue du Dr Roux 75724 PARIS Gedex 15, France. — mail: Igarnier@pasteur.fr Submitted on behalf of the Mycobacterium bovis sequencing teams, TB Research Group, Veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EX248334 BX24833

BX248334.1 GI:31616762

complete genome.

Mycobacterium bovis subsp. bovis AF2122/97

Mycobacterium bovis subsp. bovis AF2122/97

Mycobacterium bovis subsp. bovis AF2122/97

Corymebacteriae; Mycobacteriacee; Mycobacterium; Mycobacterium

tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                         1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleFroIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The complete genome sequence of Mycobacterium bovis Online Publication
341957
132
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNAS 10.1073/pnas.1130426100 (Microbiology )
2 (bases 1 to 343050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152177 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 152212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
Length:
Matches:
Conservative:
Mismatches:
                                                                                                                           Indels:
                                                                                                                                                                                                               US-09-684-215B-4 (1-132) x BX842572 (1-341957)
```

```
/gene="dhaA"
/locus tag="Mb0001"
/locus tag="Mb0001"
/locus tag="Mb0001"
/locus tag="Mb0001, dhaA, len: 507 aa. Equivalent to Rv0001,
/note="Mb0001, dhaA, len: 507 aa. Equivalent to Sv0001,
len: 507 aa, from Mycobacterium tuberculosis strain H37Rv,
len: 507 aa, from Mycobacterium tuberculosis strain H37Rv,
(99.6% identity in 507 aa overlap). dnaA, chromosomal
replication initiator protein (see citations below)
initiator protein (see citations below)
replication initiator protein (see citations below)
initiator Protein (502 aa); p49990 | DNAA MYCDA
Mycobacterium paratuberculosis (509 aa); P49990 | DNAA MYCAV
from Mycobacterium avium (508 aa); P49990 | DNAA MYCAV
from Mycobacterium avium (508 aa); p49991 | DNAA MYCAV
from Mycobacterium avium (504 aa); p49992 | DNAA MYCAV
from Mycobacterium avium (604 aa); p22H76 | DNAA STRRE from
Streptomyces reticuli (643 aa); p02H76 | DNAA STRRE from
Streptomyces reticuli (643 aa); p02H76 | DNAA STRRE from
Streptomyces reticuli (643 aa); p02H76 | DNAA STRRE from
Streptomyces reticuli (643 aa); p02H76 | DNAA STRRE from
Streptomyces reticuli (643 aa); p02H76 | DNAA STRRE from
Streptomyces reticuli (643 aa); p05H76 | DNAA STRRE
chromosomal replication initiator protein from Escherichia
coli strain K12 (467 aa); PASTA scores: Contains PS00017
ATP/GTP-binding site motif A (P-loop) and PS01008 DnaA
protein signature: BELONGS TO THE DNAA FAMILY. Note that
the first base of this gene has been taken as base 1 of
the Mycobacterium bovis genomic sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / LTAISLAL TOTAL T
Laboratories Agency Weybridge, Woodham Lane, New Haw, Addlestone, Surrey KTI5 3NB, UK. Sanger Centre, Wellcome Trusts Genome Campus, Hinxton, Cambridge CB10 LBA, UK. PT4 Annotation, Genopole, Institut Pasteur, 28 Rue du Docteur Roux, 75724 Paris Cedex 15, France. Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/evidence=experimental
/trans1_table=1!
/product="CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA"
/protein_id="CAD92863.1"
/db_xref="GI:31616763"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .343050
/organism="Mycobacterium bovis subsp. bovis AF2122/97"
/mol_type="genomic DNA"
/strain="AF2122/97"
/db_xref="taxon:233413"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /locus tag="Mb0002"
2052. 3260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="dnaA"
locus tag="Mb0001"
.1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2052. .3260
/gene="dnaN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
```

CDS

/genearreck.
//genearreck.
//g P21174 DP3B_MICLU from Micrococcus luteus (310 aa); P55023 IP33 SYNP7 from Synechococcus sp. strain PCC 7942 (375 aa); efc. Overlaps and extends CDS in neighbouring cosmid MICY1044.01." /Jocus tag="Mb0003" 3280. .4437 /gene="recF" 3280. .4437 /gene="recF"

> gene CDS

gene="dnaN"

```
Tobases I to 447)
Reed, S.G., Skelky, Y.A. W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for diagnosis of tuberculosis
Patent: US 6338852-A 4 15-JAN-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT 20-APR-2002
                        Unclassified.

Unclassified.

1 (bases 1 to 447)
Reed, S.Gaixy, A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for immunotherapy and diagnosis of tuberculosis and methods for immunotherapy and diagnosis of tuberculosis in Twards for immunotherapy and diagnosis of tuberculosis of tuberculosis for immunotherapy and diagnosis of tuberculosis of tuberculosis for immunotherapy and diagnosis of tuberculosis.

Incation/Qualifiers

Incation/Qualifiers

Incation/Qualifiers

Incation/Qualifiers

Incation/Qualifiers

Incation/Qualifiers

Incation/Qualifiers

Incation/Qualifiers

Incation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 GlyHisHisBroGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGGCACGACGAGGCGGCACGT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCGTTCAT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 IleThralaValaspGlyAlaProlleAsnSeralaThralaMetalaAspAlaLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ACGGCCGCGTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGCAATTCGCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlalleFroIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGrySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                 4447
1131
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AR182442
Sequence 4 from patent US 6338852.
AR182442
AR182442.1 GI:20225649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .447
/organism="unknown"
/wol_type="unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-4 (1-132) x AR169152 (1-447)
                                                                                                                                                                                                                                                                                                                                    3.59e-42
670.00
99.24%
99.24%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown.
                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
AR182442
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
SOURCE
ORGANISM
                                                          REFERENCE
AUTHORS
                                                                                                                                                                JOURNAL
FEATURES
                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 & 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $ B $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                              //gene="978"
/locus tag="Mb0005"
5123. 7267
/gene="978"
/locus tag="Mb0005"
/locus tag="Mb0005"
/noce="Mb0005, 9728, len: 714 aa. Equivalent to Rv0005, noce="Mb0005, 9728, len: 714 aa. from Mycobacterium tuberculosis strain H37Rv, 199.9$ identity in 714 aa overlap). gyrB, DNA gyrase subunit B (EC 5-99.1.3) (see citations below), equivalent, except in N-terminus, to other Mycobacterium leprae (697 aa); gylD113|GYRB MYCRA from Mycobacterium avium subsp. paratuberculosis (677 aa) (has its N-terminus shorter); p48355|GYRB MYCSM from Mycobacterium snegmatis (675 aa); etc. Also highly similar to others e.g. T10069 from Streptomyces coelicolor (686 aa); P50075|GYBS_STRSH from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GICCAACGCGIGGICGGGAGCGCTCCGGCGGCAACTCTCGGCATCTCCACCGGCGACGTG 152247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 17-DEC-2001
      /codon_start=1
/transl_table=11
/product="CONSERVED HYPOTHETICAL PROTEIN"
/product="CONSERVED HYPOTHETICAL PROTEIN"
/product="CAD92866.1"
/db_xref="G1:31616766"
/dc_xref="G1:3161676"
/dc_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlyGerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152128 ATGGGGCCTACCGCCTTCCTCGGCTTGTCGACAACAACAACGGCAACGGCGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValGInArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlvGlvGlvGlvPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343050
132
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AR169152 447 bp
Sequence 4 from patent US 6290969.
AR169152 AR169152.1 GI:17906927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-4 (1-132) x BX248334 (1-343050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.12e-39
675.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
AR169152
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment S
Pred. No.:
                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
```

100

250

80

190

9

70 40

The content of the co

PAT 21-JUN-2002

DNA

```
AX429596
                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                 AX832581
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                       REFERENCE
AUTHORS
                                                                                          JOURNAL
                                                                            TITLE
                                                                                                                                           ORIGIN
                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                  8 8 8
                                                                                                                                                                                                                                                                                                            8 B 8
                                                                                                                                                                                                                             ò
                                                                                                                                  ISM Unclown.

Unclassified.

Unclassified.

Unclassified.

Unclassified.

Unclassified.

RS Red, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C.

Compounds and methods for immunotherapy and diagnosis of tuberculosis

Uncertical Science of the Compounds of the Compounds of tuberculosis of tuberculosis

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                     250
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 17-AUG-2003
                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                          310
                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                            4447
1131
1
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                           AR353302 4 from patent US 6592877. AR353302. GI:33759108
                                                                                                                                                                                                                                                                                            US-09-684-215B-4 (1-132) x AR353302 (1-447)
                                                                                                                                                                                                                                            3.59e-42
670.00
99.24*
99.24*
99.26*
                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
Score:
Forcent Similarity:
Best Local Similarity:
Ouery Match:
69
                                                                                                                           .
Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371
                                                                                                                                                                                                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                     251
                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
           251
                                                                              RESULT 17
AR353302
LOCUSTON
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 18
AX429596
                                                                                                                                                                                     JOURNAL
FEATURES
                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                        TITLE
                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                       के विकं
                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                         8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                S B
                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                      \delta
                     6 6 6
                                                              ρp
```

```
reed, S.G., Skeiky, Y.A., Dillon, D.C., Campos-Neto, A., Houghton, R.L., Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for immunotherapy and diagnosis of tuberculosis
Patent: EP 1203817-A 4 08-MAY-2002;
CORIXA CORPORATION (US)
Location/Qualifiers
1. 447
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310
                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                 70
                                                                                                                                                                                                                                                                                                                             linear PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reed, S.G., Skeiky, Y.A., Campos-Neto, A., Houghton, R.L.,
Vedvick, T.S., Twardzik, D.R. and Dillon, D.C.
                                                                                                                                                                                                                                      4447
131
10
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AX832581 from Patent EP1347055.
AX83281
AX832581.1 GI:39840631
447 bp
4 from Patent EP1203817.
                                                                                                                                                                                                                                                                                                            US-09-684-215B-4 (1-132) x AX429596 (1-447)
            Sequence 4 from Patent 1
AX429596
AX429596.1 GI:21540845
                                                                                                                                                                                                                                    3.59e-42
670.00
99.24%
99.24%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified
unidentified
unclassified.
                                                  unidentified
unidentified
unclassified.
                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
```

```
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BD006445
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                 source
                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                   Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                        8 8
                                                                                                                                                                                                                                                                                                                                                                                                                   8 & 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                               81 ileThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                               08/818111 PI
ANTONIO CAMPOS
                                                                                                                                                                                                                                                                                             BDD06325

ON Compounds and methods for diagnosis of Tuberculosis.

N BD066325.1 GI:18634696

Unidentified

SM unidentified

unclassified.

L (bases 1 to 447)

E 1 (bases 1 to 447)

Vedvick, T.S., Twardzik, D.R. and Lodes, M.J.

Compounds and methods for diagnosis of Tuberculosis

L Patent: JP 2001500383-A 4 16-JAN-2001;
                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                   ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlylleSerThrGlyAspVal 80
                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                    70
                                                                                                                                                                                                                             GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerFroThrValHis
                                                                                                                                                                                                                                                                                                                        41 IleGlyProThrAlaPheLeuGlyLeuGlyValValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
Compounds for immunotherapy and diagnosis of tuberculosis Patent: EP 1347055-A 4 24-SEP-2003; CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAYMOND HOUGHTON, THOMAS S VEDVICK, DANIEL R TWARDZIK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OS Unidentified
PN JP 2001500383-A/4
PD 16-JAN-2001
PF 07-CCT-1997 JP 1998518432
PR 11-CCT-1996 US 08/729622,13-MAR-1997 US
STENCH G REED, YASIR A W SKRIKY, DAVIN C DILLON, PI
NETO,
                                                                                                                            4447
1131
0 0
0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGGCC 406
                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:

    .447
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                         US-09-684-215B-4 (1-132) x AX832581 (1-447)
                                    Location/Qualifiers
                                                                                                                            3.590-42
670.00
99.24%
99.26%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MICHAEL J LODES
                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                  Scores:
                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 20
BD006325
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOUNCE
ORGANISM
                                                  source
                                                                                                                 Alignment S
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
   TITLE
JOURNAL
                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                            DRIGIN
                                                                                                                                        Score:
```

ò g δ g à g à g 8 9 ò 셤 à g

```
Compounds and methods for immunotherapy and diagnosis of Tuberulosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGGCGCACGCGT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N BD006445

BD006445.1 GI:18634816

JP 2001501832-A/4.

Unidentified

Unclassified.

B (Compounds and methods for immunotherapy and diagnosis of Patent: JP 2001501832-A 4 13-FEB-2001;

COMINGENTIFIED CORP.

COMINGENTIFIED CORP.

COMINGENTIFIED CORP.

COMPOUNDS A DESTRUCTION OF THE CORP.

CORP. OF THE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
PC C12N15/31,C07K14/35,C07K16/12,C12Q1/68,C12N15/62,G01N33/53
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source | 1.447
| /organism='Unidentified'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 ATCGGGCCTACCGCCTTCCTCGCCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 Acceccecercearaacriccaecrerccaecreseseseseseseserresearreseare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 erccaacecereerceeaacecreceeceacaacereceecarereceecarecee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IleThralaValAspSlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. 447
/mol type="genomic DNA"
/mol type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-684-215B-4 (1-132) x BD006325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.59e-42
670.00
99.24%
99.24%
```

ပ္ပ

```
Compounds and methods for immunotherapy and diagnosis of tuberculosis.

BD069285.1 GI:22614888

JP 2001517069-A/4.
                                                         CI2N15/31, C07K14/35, A61K39/04, A61K48/00, A61K49/00, C12N15/62, C07K19/00, G01N33/60, G01N33/60, G01N33/569, C12N1/19, C12N1/20, C12N1/21, PC
 ANTONIO CAMPOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 ATCGGGCCTACCGCCTTCCTCGGCTTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 GICCAACGCGIGGICGGGAGCGCTCCGGCGAAGICICGGCAICTCCACCGGCGACGIG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAAACCAAGTCGGGCGGCACGGT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 447)
Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R.,
Vedvick, T.H. and Twardzik, D.R.
                            PI RAYMOND HOUGHTON, THOMAS S VEDVICK, DANIEL R TWARDZIK, PI MICHAEL J LODES
 ď
STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON,
                                                                                                                                                                                                                                                                                                                                               4447
1131
10
0
0
0
                                                                                                                                                                                      ce 1. .447
/organism='Unidentified'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 ACAGGAACGTGACATTGGCCGAGGGACCCCCGGCC 406
                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                       Location/Qualifiers

    .447
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1-447)
                                                                                                               (C12N1/21,C12R1:19)
Strandedness: Single;
Topology: Linear;
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-4 (1-132) x BD006445
                                                                                                                                                                                                                                                                                                                                            3.59e-42
670.00
99.24%
99.24%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unclassified.
                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                           PC C12N1E
PC C07K19
PC C01N3
C12N5/10//
PC C12N/
CC Stranc
CC Topolc
FH Key
                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 22
BD069285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
```

```
PAT 17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGGGGCACGGT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ThralaalaaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 ATCGGGCCTACCGCCTTCCTCGGCTTGGCTGTTGTCGACAACAACAACGCAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 GTCCAACGCGTGGTCGGGGGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
                                                                                                                                                                                                7,10,
Cl2N1/21//A61K39/04, (Cl2N1/21, Cl2R1:19)
Strandedness: Single;
Topology: Linear;
Compounds and methods for immunotherapy and diagnosis of
tuberculosis
Compounds and methods for immunotherapy and diagnosis of Patent: JP 2001517069-A 4 02-OCT-2001; CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BD205817
447 bp DNA linear E compounds and methods for diagnosis of tuberculosis.
BD205817
                                                                                                                                                                                                                                                                                                                                                                                                                             440
480
71
                                                                                                                                                                                                                                                                                                /organism='Unidentified'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 1. .447
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-4 (1-132) x BD069285 (1-447)
                                                                                                                                                                                                                                                                                            .447
                                                                                                                                                                                                                                                                                                                                                                                                                          3.59e-42
670.00
99.24*
99.24*
                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                            FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 23
BD205817
                                                                                                                                                                                                                                                                                                                    FEATURES
                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
```

```
Unclassified.

1 (bases 1 to 1872)
Reed,S.G., Skeiky,Y.A.W., Dillon,D.C., Campos-Neto,A., Houghton,R., Vedvick,T.S. and Twardzik,D.R.
Compounds and methods for immunotherapy and diagnosis of tuberculosis
Patent: US 6290966-A 17 18-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-2002
                                                                                                                                                                   PAT 17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGGCACGCGT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThralaalaaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPhealaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1872
131
0
1
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acadedaacerdacarredeceaadedececedece 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                              371 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC
                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AR182455 1872 bp
Sequence 17 from patent US 6338852.
AR182455 AR182455.1 GI:20225662
                                                                                                                                                                 AR169165
Sequence 17 from patent US 6290969.
AR169165.1 GI:17906947
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. 1872
/organism="unknown"
/mol_type="unassigned Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-684-215B-4 (1-132) x AR169165 (1-1872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.496-41
670.00
99.248
99.248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                 .
Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AR182455
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                      AR169165
LOCUS
                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       а
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                       d
                                   8
RONALD C HENDRICKSON
C12X15/09, C07H21/02, C07H21/04, C07K7/00, C07K14/35, C07K16/12, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C07K19/00, C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/04, C12Q1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAAACGGCAACGGCGCACGA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 erccaacecereerceercecerceecececececeaercreecarcreecarececeaecere 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 Acceccecerceanhaachrecaechereceaegreseaagaanresecannessane 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAYMOND HOUGHTON, THOMAS S VEDVICK, DANIEL R TWARDZIK, MICHAEL
                                                                                                                                                                                                                                                                                                                                         PF 17-FEB-1999 JP 2000532132
PR 18-FEB-1998 US 09/024753,05-MAY-1998 US 09/072596 PI
STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCACCGCGGTCGACGGCGCTCCGATCACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .447
1. Organism="Mycobacterium tuberculosis"
| Companism="Mycobacterium tuberculosis" | Mol type="genomic DNA" | Mol type=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447
0 131
0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis
JP 2002530050-A/4
17-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-4 (1-132) x BD205817 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.59e-42
670.00
99.24%
99.26%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C07K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
```

g

8 8 8

ò 8 임

음 강

877

817

40

937

80

```
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Alignment Scores:
Pred, No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 27
AR233110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                     원
                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                    쉺
                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                 ð
                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGGTGGCGGACGCGCTTAAC 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1058 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGCGCACGCGT 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 20-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                    1 (bases 1 to 1872)
Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R. Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for diagnosis of tuberculosis
Patent: US 6338652-A 17 15-JAN-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         GTCCAACGCGTGGGAAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 997
                                                                                                                                                                                                                                                                                                                                          758 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 817
                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                    41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                                                                                                                                                                                                                                                                                                                                                                  GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unclassified.

1 (bases 1 to 1872)

Reed, 5G., Skeiky, Y.A.W. and Dillon, D.C.

Compositions and methods for the prevention and treatment of M. tuberculosis infection

Patent: US 6350456-A 17 26-FEB-2002;
                                                                                                                                                                                                                                                                                                             1 ThralaalaaseraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                           1872
131
0
1
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1118 ACAGGGAACGIGACAIIGGCCGAGGGACCCCCGGCC 1153
                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 from patent US 6350456. AR194838 AR194875
                                                                                                                  1. ,1872
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="unassigned DNA"
                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                    US-09-684-215B-4 (1-132) x AR182455 (1-1872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .1872
/organism="unknown"
                                                                                                                                                                                           1.49e-41
670.00
99.24%
99.24%
            Unknown.
Unclassified.
                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown.
 Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown
                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 26
AR194838
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                                                                                                                   source
         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                       TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                       REFERENCE
                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                               \delta
                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
1 (bases I to 1872)
Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C. Compounds and methods for diagnosis of tuberculosis
Patent: US 6458366-A 17 01-CT-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT 20-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 ileThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                  817
                                                                                                                                                                                                                                                  877
                                                                                                                                                                                                                                                                                                                  937
                                                                                                                                                                                                                                                                                                                                                                                997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                   1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                  758 Acceccecciccanaacriccaecrerecaeegreeecaeegaricecariccearic
                                                                                                                                                                                                                21 GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlyGerProThrValHis
                                                                                                                                                                                                                                     41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                  878 Arceseccracceccrrccrcescrrescretreresacaacaacaaceacaaceacaacea
                                                                                                                                                                                                                                                                                                                                                ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                  938 drechaededregredahadedereededeharereedehrereekeedekeera
                                                                                                                                                                                                                                                                                                                                                                                                                                        101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1872
131
0
1
0
0
   1872
131
0
1
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1118 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                 Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
   Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1872 bp 1
Sequence 17 from patent US 6458366.
AR233110
AR233110.1 GI:27275546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .1872
/organism="unknown"
/mol_type="genomic DNA"
                                                                                     Gaps:
                                                                                                                   US-09-684-215B-4 (1-132) x AR194838 (1-1872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-4 (1-132) x AR233110 (1-1872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.49e-41
670.00
99.24%
99.24%
1.49e-41
670.00
99.24%
99.24%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
DB:
```

us-09-684-215b-4.rge

rage to

Db 998 ATCACCOCGGTCGACCACTCGGACCACCGCGATGGCGGTTAAC 1057 Cy 101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyGlyThrArg 120 Db 1058 GGCATCATCCGGTGACGTCATCACGGTGAACTGGCAAGTCGGGACGCGT 1117 Cy 121 ThrGl	## Alignment Scores: 1.49e-41 Length: 1872 131
0y 111eGlyProThArlanelaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40 22 GGGCAGGCGATGGCGCAAACCGAACCGACCACCCACCCAC	AUTHORS Read, S.G., Steiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C. Compounds and methods for immunotherapy and diagnosis of tuberculosis source Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers (Mol_type="genomic DNA") Alignment Scores: 1.49e-41 Length: 1872 131 1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872 1.1872

PAT 12-DEC-2003 938 GTCCAACGCGTGGTCGGAAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGAAGGGG 997 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60 Leed, S.G., Skeiky, Y.A., Campos-Neto, A., Houghton, R.L., Vedvick, T.S., Twardzik, D.R. and Dillon, D.C.
Compounds for immunotherapy and diagnosis of tuberculosis Patent: EP 1347055-817 24-SEP-2003;
CORIXA CORPORATION (US)
Location/Qualifiers
1. 1872
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644" Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: DNA AX832594 1872 bp Sequence 17 from Patent EP1347055. AX832594.1 GI:39840644 US-09-684-215B-4 (1-132) x AX832594 (1-1872) 1.49e-41 670.00 99.24% 99.24% unidentified unidentified unclassified Score:
Percent Similarity:
9
Best Local Similarity:
9
Query Match:
6
DB: Alignment Scores: Pred. No.: RESULT 30
AX832594
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
SEYWORDS
SOURCE
ORGANISM FEATURES Source TITLE JOURNAL REFERENCE AUTHORS ORIGIN a ð d ò d à d à В ਨੇ d ઠ

Search completed: April 30, 2004, 02:24:00 Job time : 3854.74 secs

2 00.00.00 4

mon may

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

April 29, 2004, 22:43:07; Search time 109.952 Seconds (without alignments) 1234.209 Million cell updates/sec Published Applications NA:*

| cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/CTT NW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:* OM protein - nucleic search, using frame_plus_p2n model TAASDNFQLSQGGGFAIPIGQAMAIAGQI 30 Total number of hits satisfying chosen parameters: 2936184 segs, 2261732022 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext US-09-684-215B-17 148 1 TAASDNFQLSQGGQGI Minimum DB seq length: 0 Maximum DB seq length: 2000000000 **BLOSUM62** Title: Perfect score: Scoring table: Database : Sequence: Searched: Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query No. Score Match Length DB ID

Description

20000000	duence 1877 equence 1876 equence 1887 equence 1887 equence 235 quence 353 quence 353 quence 354 quence 834 quence 834 quence 834 quence 834
19 - 9 - 9 - 9 - 9 - 9 - 9 - 9 - 9 - 9 -	0.05-10/113-67.2-180.0 0.05-09/2-941-1807.0 0.05-09-90.2-941-1807.0 0.05-09-90.2-941-1807.0 0.05-09-90.4-45.0 0.05-09-90.4-45.0 0.05-09-90.4-45.0 0.05-09-90.4-45.0 0.05-09-90.7-05-35.0 0.05-09-90.7-05-35.0 0.05-09-90.7-05-35.0 0.05-09-90.7-09-35.0 0.05-09-90.7-09-95.0 0.05-09-90.8-35.0 0.05-09-80.8-35.0 0.05-09-80.8-35.0 0.05-09-80.8-35.0 0.05-09-80.8-35.0 0.05-09-80.8-35.0 0.05-09-80.8-35.0 0.05-09-80.8-35.0 0.05-09-80.8-35.0 0.05-09-80.8-35.0 0.05-09-80.8-35.0 0.05-09-80.8-35.0 0.05-09-80.8-35.0 0.05-09-80.8-33.8-34.0 0.05-09-80.8-33.8-34.0 0.05-09-80.8-33.8-34.0 0.05-09-80.8-33.8-34.0 0.05-09-80.8-33.8-34.0 0.05-09-80.8-33.8-34.0 0.05-09-80.8-33.8-34.0 0.05-09-80.8-33.8-34.0 0.05-09-80.8-33.8-34.0 0.05-09-80.8-34.8-34.0
1186 1186 1186 1186 1186 1186 644 1444 14	
: ਜੋਨੇਜੋਜੋਜੋਜੋਜੋਜੋਜੋਜਜਜਜਜਜਜਜਜਜਜਜਜਜਜਜ !	000000000000000000000000000000000000000
	* * * * * * * * * * * * * * * * * * * *
	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7

ALIGNMENTS

```
Sequence 1979, Application US/09902941

Patent No. US200020172952A1

GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Warg, Tongtong
APPLICANT: Marcanabe, Yoshihiro
APPLICANT: Retter, Marc W.
APPLICANT: Rederick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Gary R.
APPLICANT: Wondow, Chaitanya S.
APPLICANT: Wondows. Chaitanya S.
APPLICANT: Wondows. Chaitanya S.
APPLICANT: Wondows. Marcia
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITILE OF INVENTION: COMPOSITIONS AND LIARRAPY
ITILE OF INVENTION: COMPOSITION WOMBER: US/09/902,941

CURRENT APPLICATION NUMBER: US/09/902,941

CURRENT APPLICATION NUMBER: US/09/902,941

CURRENT APPLICATION NUMBER: US/09/902,941

CURRENT APPLICATION WINDOWS Version 4.0
```

```
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGCCAGGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                                                1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                          22 ACGGCCGCGTCCCATAACTTCCAGCTGTCCCAGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1879, Application US/09849626

Publication No. US20020197669A1

GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya
APPLICANT: Bangur, Gary
APPLICANT: Wang, Aijun

APPLICANT: Wang, Tongtong
APPLICANT: Wang, Aijun

APPLICANT: Wang, Congroud
APPLICANT: Clapper, Jonathan

TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: DIAGNOSIS OF LUNG
CURRENT APPLICATION NUMBER: US/09/849,626

CURRENT FILING DATE: 2010.105-03

NUMBER OF SEQ ID NOS: 1926

SEQ ID NO 1879

LENGTH: 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        00000
00000
                                                                                                                       186
30
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-215B-17 (1-30) x US-09-849-626-1879 (1-186)
                                                                                                                                                                                                                                             US-09-684-215B-17 (1-30) x US-09-902-941-1879 (1-186)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                 21 GlyGlnAlaMetAlaileAlaGlyGlnile 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-10-283-017-1879
Sequence 1879, Application US/10283017
Publication No. US20030211510A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.99e-16
148.00
100.00%
100.00%
                                                                                                                       1.99e-16
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-849-626-1879
; SEQ ID NO 1879
; LENGTH: 186
; TYPE: DNA
; OKGANISM: Homo sapiens
US-09-902-941-1879
                                                                                                                                          Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-849-626-1879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                          Alignment Scores:
                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                 ð
```

```
APPLICANT: Main and APPLIC
```

us-09-684-215b-17.rnpb

```
1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaileProile 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCGATC 81
                                                                                                                                                                          20
                                                                                                                                                                                              22 ACGGCCGCGTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCCGTTC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-09-757-417-46
US-09-757-417-46
Squence 46, Application US/09757417
Squence 46, Application US/09757417
GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
STILE REFERENCE: 210121.479C1
CURRENT APPLICATION NUMBER: US/09/757,417
                                                                                                                                                                                                                                                                                                                                                         Sequence 1879, Application US/10113872
; Sequence 1879, Application US/10113872
; Publication No. US2003017025541
; GREERAL INFORMATION:
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Salos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Darrick
; APPLICANT: Carter, Darrick
; APPLICANT: Carter, Darrick
; APPLICANT: Panger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND NETHODS FOR THE THERAPY
; TITLE OF INVENTION: COMPOSITIONS
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; TITLE OF SEQ ID NOS: 2011
; SOFTWARER: FASTERQ for Windows Version 4.0
; SEQ ID NO 1879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186
00000
  186
000
000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Gaps:
Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-684-215B-17 (1-30) x US-10-113-872-1879 (1-186)
                                                                                                                                   US-09-684-215B-17 (1-30) x US-10-017-754-1879 (1-186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.99e-16
148.00
100.00%
100.00%
1.99e-16
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-10-113-872-1879
Score: 1.
Score: 1.
Percent Similarity: 1.0
Query Match: 1.0
DB: 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                            RESULT 5
US-10-113-872-1879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                 d
```

```
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7

US-10-042-945-46

| Sequence 46, Application US/10042945
| Publication No. US20030045468A1
| GENERAL INFORMATION:
| APPLICANT: Pling, Steven P. |
| APPLICANT: Pling, Steven P. |
| APPLICANT: Glapper, Jonathan D. |
| APPLICANT: Wang, Aljun |
| APPLICANT: Wang, Aljun |
| APPLICANT: Wang, Aljun |
| APPLICANT: Woneon, Jeffrey C. |
| APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-684-215B-17 (1-30) x US-10-042-945-46 (1-399)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-17 (1-30) x US-09-757-417-46 (1-399)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
; CURRENT FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 399
; TYPE: DN Am
; ORGANISM: Homo sapiens
US-09-757-417-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-10-193-002-4
; Sequence 4, Application US/10193002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.77e-16
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                   4.77e-16
148.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                Score:
Percent Similarity: 10
Best Local Similarity: 10
Query Match: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
```

```
Skeiky, Yasir A.W.

Dillon, Davin C.

Campoe Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 COLUMDIA Center, 701 Filth Avenue
CITY: Saattle
STATE: Washington
COMPUTER: 19104-7092
COMPUTER: Palot4-7092
COMPUTER: Palot4-7092
COMPUTER: Palot6 Compatible
COMPUTER: Palot6 Compatibl
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                     Skeiky, Yaair A.W.
Skeiky, Yaair A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPONDOS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS: 350
CORRESPONDENCE ADDRESS: ADDRESSES: REATE ADDRESSES: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSITCATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-199
ATTORNEY/AGENT INFORMATION:
REFIREMENCE/DOCKET NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEPAX: (206) 622-4900
TELEPAX: (206) 622-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444
000
000
000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-17 (1-30) x US-10-193-002-4 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.44e-16
148.00
100.00%
100.00%
                    Publication No. US20030135026A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-193-002-4
```

```
## SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-084-843-4

Alignment Scores:

Pred. No.:

1447

Alignment Scores:

148.00

Bred. No.:

148.00

Conservative:

Conservative:
```

ò

RESULT 9
US-10-084-843-4
; Sequence 4, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:

us-09-684-215b-17.rnpb

```
1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 Aceccecerceanaacriceaererereceaeereeecaearreecarreceare
                                                                                                                                                                                                                                                22 Accecedenceannacriceaecrenceaecreecaecaecaecarreecanreecanc
                                                                                                                                                                                                       1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlyGlyBheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Aljun
APPLICANT: Steiky, Yasir A.W.
APPLICANT: Steiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Horal, Juliam
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION WHEER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH. 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     675
000
000
000
  80000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-684-215B-17 (1-30) x US-09-780-669-822 (1-675)
                                                                                                                                                    US-09-684-215B-17 (1-30) x US-09-759-143-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCAGGCGATGCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                            21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                        21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 822, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitcham, Javin C.

Mitcham, Javin C.

Mitcham, Jennifer L.

Harlocker, Susan L.

Jiang, Yuqui
Henderson, Robert A.

Ralos, Michael D.

Raper, Gary R.

Retter, Marc W.

Stolk, John A.

Day, Craig H.

Vedvick, Thomas S.

Carter, Darrick

Li, Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.73e-16
148.00
100.00%
100.00%
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-780-669-822
     Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-780-669-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 ACGGCCGCCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a FILLE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR PILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 9
LENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ALL OLDINO, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Garry R.
APPLICANT: Fanger, Garry R.
APPLICANT: Retter, Marc W.
APPLICANT: Carter, Darrick
APPLICANT: Oraig H.
APPLICANT: Wang, Ajun
APPLICANT: Wang, Ajun
APPLICANT: Mang, Ajun
APPLICANT: Garrick
APPLICANT: Carter, Darrick
APPLICANT: Oraig H.
APPLICANT: Wang, Ajun
APPLICANT: Seeiky, Yasir A.W.
APPLICANT: Oraig H.
APPLICANT: Seeiky, Yasir A.W.
APPLICANT: Oraig H.
APPLICANT: Seeiky, Yasir A.W.
APPLICANT: Seeiky, Yasir A.W.
APPLICANT: Seeiky, Yasir A.W.
APPLICANT: Seeiky, Yasir A.W.
APPLICANT: Wang, Ajun
                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:WIBRal2 (WTB32A;
OTHER INFORMATION: C-terminus)
US-10-098-732A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444
330
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-17 (1-30) x US-10-098-732A-9 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 GGGCAGGCGATGGCGATCGCGGGCCAGATC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 822, Application US/09759143
Patent No. US2002022248A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.44e-16
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.73e-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-759-143-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity: 1
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                      22 ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                          1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGJyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
TILLE ON INVENTION: CARLY R.
TILLE OF INVENTION: CARLY R.
TILLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427026
CURRENT APPLICATION NUMBER OF 29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         675
30
00
00
00
                                                                         675
000
000
000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-684-215B-17 (1-30) x US-09-895-814-822 (1-675)
                                                                                                                                                                                                                   US-09-684-215B-17 (1-30) x US-09-895-793-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                                              82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                         21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-895-814-822

; Sequence 822. Application US/09895814

; Publication No. US20020193296A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ku, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Mitchael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Dayres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
                                                                       8.73e-16
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-09-895-814-822
; ORGANISM: Homo sapiens
US-09-895-793-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                     Best Local Similarity:
Query Match:
                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .22 ACGCCCCCCTCCCATAACTTCCCAGCTCTCCCAGGGTGGCCAGAGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
    Sequence 812, Application US/09822827

Patent No. US20020081680A1

GENERAL INCRNATION:
APPLICANT: Xu. Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534827

CURRENT APPLICATION WHORER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

SECOND NOS: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FOY, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895, 793
CURRENT APPLICATION NUMBER: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                  675
00
00
00
00
                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-684-215B-17 (1-30) x US-09-822-827-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 GGGCGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 822, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wi. Jiangchun
APPLICANT: Mitchan, Jennifer L.
APPLICANT: Mitchan, Jennifer L.
APPLICANT: Arlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
                                                                                                                                                                                                                                                                                                                                                                          8.73e-16
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-822
                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-09-822-827-822
                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
```

엄 à

```
TYPE: DNA
) ORGANISM: Homo sapiens
US-10-294-025-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-678A-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 18
US-10-294-025-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 81
22 ACGCCCCCCCCATAACTTCCAGCTGTCCCAGGGTGGCCAGGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DAGNOSIS OF PROSTATE CANCER
FILE REPREADE 2100.11.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         675
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-684-2158-17 (1-30) x US-10-012-896-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 GGGCAGGCGATGCGGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                              82 ececacearecearcecececeant
                                          21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-144-678A-822
Sequence 822, Application US/10144678A
Publication No. US220030157089A1
GENERAL INFORMATION:
                                                                                                                                                                 Sequence 822, Application US/10012896; Publication No. US20020183251A1; GENERAL INFORMATION:
                                                                                                                                                                                                                             APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Xalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Garter, Darrick
APPLICANT: Ii, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CRGANISM: Homo sapiens
US-10-012-896-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 17
```

g

ઠે 셤 ò

```
22 ACGGCCGCGTCCCGATAACTTCCAGGCTGTGCCAGGGTGGGCAGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ThralaalaseraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 822. Application US/10294025
; Publication No. US20030185830A1
; Publication No. US20030185830A1
; GENERAL INFORMATION:
    APPLICANT: Xu, Jiangchun A.
    APPLICANT: Stolk, John A.
    APPLICANT: Stolk, Joh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOR THE THERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            675
00
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MCMEIL, WOUNT
APPLICANT: MCMEILL, WEARCHED D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: UNDER: US/10/144,678A
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FREISEQ for Windows Version 3.0
SEQ ID NO SEASOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-684-215B-17 (1-30) x US-10-144-678A-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 édechédedehrédedehredededechéhre 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, Aijun
Skeiky, Yasir A. W.
Hepler, William T.
Hural, John
arlocker, Susan L.
iang, Yuqiu
                                                                                                                                                                                                                                                                                                                  Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.73e-16
148.00
100.00%
100.00%
```

```
US-10-359-460-27, Application US/10359460

Publication No. US20030147911A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Blion, Davin C.

APPLICANT: Alderson, Mark

APPLICANT: Campos-Netc, Antonio

PRIOR PLING DATE: 1999-04-07

PRIOR FILING DATE: 1999-04-07

PRIOR FILING DATE: 1999-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR PRIOR PRIOR DATE: 1998-04-07

PRIOR PRIOR DATE: 1998-04-07

PRIOR PRIOR PRIOR DATE: 1998-04-07
                                                                                                                                        25 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTCGGCAGGGATTCGCCATTCCGATC
                                                                                              1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:bi-fusion OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading OTHER INFORMATION: frame 1 FRATURE:
NAME/KEY: CDS
LOCATION: (1)...(693)
LOCATION: (1)...(693)
LOCATION: (2)...(693)
OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24), OTHER INFORMATION: reading frame 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           707
000
000
000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                            US-09-684-215B-17 (1-30) x US-09-287-849-27 (1-702)
                                                                                                                                                                                                                                                                                        85 GGCAGGCGATGCCGATCGCGGGCCAGATC 114
                                                                                                                                                                                                                         21 GlyGlnAlaMetAlaileAlaGlyGlnile 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(700)
OTHER INFORMATION: reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:

NAME/KEY: CDS

LOCATION: (3)..(701)

OTHER INFORMATION: reading frame
US-10-359-460-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.13e-16
148.00
100.00%
100.00%
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/09287849

Sequence 27, Application US/09287849

Patent No. USZO020009459A1

SEGUENCE 21, Application US/09287849

Patent No. USZO020009459A1

SEGUENCE 21 USPANTION:

APPLICANT: Reed, Steven G.

APPLICANT: Alderson, Mark

APPLICANT: Alderson, Mark

APPLICANT: Corrixa Corporation

TITLE OF INVENTION: And Their Uses

TITLE OF INVENTION: 1990-00-07

TITLE OF INVENTION: US 08/818,112

PRIOR FILING DATE: 1997-00-13

PRIOR PILING DATE: 1997-00-13

PRIOR PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-04-07

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 27

TURE OF NAME OF SEQ ID NOS: 46

SEQ ID NO 27

TURE OF NAME OF SEQ ID NOS: 46

SEQ ID NO 27

TURE OF NAME OF SEQ ID NOS: 46

SEQ ID NO 27

TURE OF NAME OF SEQ ID NOS: 46

SEQ ID NO 27

TURE OF NAME OF SEQ ID NOS: 46

SEQ ID NO 27

TURE OF NAME OF SEQ ID NOS: 46

SEQ ID NO 27

TURE OF NAME OF SEQ ID NOS: 46

SEQ ID NO 27

TURE OF SEQ ID NOS: 46

SEQ ID NO 27

TURE OF SEQ ID NOS: 46

SEQ ID NO 27

TURE OF SEQ ID NOS: 46

SED ID NO 27

TURE OF SEQ ID NOS: 46

SED ID NO 27

TURE OF SEQ ID NOS: 46

SED ID NO 27

TURE OF SEQ ID NOS: 46

SED ID NO 27

TURE OF SEQ ID NOS: 46

SED ID NOS: 46

                                                                                                                                                                                                                                                                                                                               1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence:bi-fusion OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading OTHER INFORMATION: frame 1
NAME/KEY: CDS
LOCATION: (1)..(693)
OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24), OTHER INFORMATION: cading frame 1
NAME/KEY: CDS
LOCATION: (2)..(700)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    702
30
0
                               675
30
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                            US-09-684-215B-17 (1-30) x US-10-294-025-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 GGGCAGGCGATGGCGATCGCGGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (3)..(701)
OTHER INFORMATION: reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.13e-16
148.00
100.00%
100.00%
                        8.73e-16
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 19
US-09-287-849-27
                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹
```

g δ 셤

```
1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaileProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bangur. Chaitanya
APPLICANT: Bangur. Gary
APPLICANT: Fanger. Gary
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C16
CURRENT PFLICATION UNMER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SOFTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 Aceccecercearaacriceaerereceaecraecres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 Acedocecercearaacriccaecrerceaedeaedeaear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           800000
                                                                                                                                                                                                                                                                                                                                                                                              857
0000
0000
                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER CURRENT APPLICATION NUMBER: US/09/902,941 CURRENT FILING DATE: 2001-07-10 NUMBER OF SEQ ID NOS: 2002 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1662 LENGTH: 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-17 (1-30) x US-09-849-626-1862 (1-822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-684-215B-17 (1-30) x US-09-902-941-1862 (1-822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                deschescearescearescesesceaeare 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 edecadecearedecearcecedeceare 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1862, Application US/09849626
Publication No. US20020197669A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           1.09e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
US-09-849-626-1862
                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-09-902-941-1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-849-626-1862
                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                    red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 ACGCCCCCTCCCATACTTCCACCTCTCCAGGTCCCCAGGGTCCCCATTCCCATCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
                                                                      1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
                                                                                                                         25 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaiteanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Pedvick, Tom
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Rannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Pan, Liqun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Liqun
APPLICANT: Wang, Liqun
APPLICANT: Wang, Aljun
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
IIILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8875
0000
0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-17 (1-30) x US-09-736-457-1862 (1-822)
            US-09-684-215B-17 (1-30) x US-10-359-460-27 (1-702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 GGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                              85 GGGCAGGCGATGGCGATCGCGGGCCAGATC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                        21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1862, Application US/09902941 Patent No. US20020172952A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        1862, Application US/09736457
5. US20020168637A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Henderson, Robert A. APPLICANT: Wang, Tongrong APPLICANT: Watanabe, Yoshihiro APPLICANT: Johnson, Jeffrey C. APPLICANT: Marnerakis, Margarita APPLICANT: Carter, Darrick APPLICANT: Fanger, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fanger, Gary R.
Vedvick, Thomas S.
Bangur, Chaitanya S.
McNabb, Andria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.09e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-09-736-457-1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
```

Query Match: DB:

d

ò

g

ઠે

CCGATC 81

```
RESULT 26
US-10-113-872-1862
| Sequence 1862, Application US/10113872
| Sequence 1862, Application US/10113872
| Publication No. US20030170255A1
| GENERAL INFORMATION:
| APPLICANT: Matemabe, Yoshihiro
| APPLICANT: Kalos, Michael D.
| APPLICANT: Rades, Michael D.
| APPLICANT: Thomas S.
| APPLICANT: Carter, Darrick
| APPLICANT: Carter,
                                                                                                                                                                                           875
30
00
00
00
                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-684-215B-17 (1-30) x US-10-017-754-1862 (1-822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 GGGCAGGCGATGCGGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyGlnAlaMetAlaileAlaGlyGlnile 30
                                                                                                                                                                                    1.09e-15
148.00
100.00$
100.00$
100.00$
      ; LENGTH: 822
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-754-1862
                                                                                                                                                                                                                                    Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                   Alignment Scores:
Pred. No.:
RESULT 24

US-10-283-017-1862

US-10-283-017-1862

Sequence 1862, Application US/10283017

Sequence 1862, Application US/10283017

Sequence 1862, Application US/10283017

Sequence 1862, Michael D.

APPLICANT: Wang, Tongtong

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Balath, Paul R.

APPLICANT: Gleath, Paul R.

APPLICANT: Grater, Marc W.

APPLICANT: Carter, Marc W.

APPLICANT: Carter, Marc W.

APPLICANT: Carter, Thomas S.

APPLICANT: Carter, Thomas S.

APPLICANT: Manger, Gary R.

APPLICANT: Manger, Chaitanya S.

APPLICANT: Manger, Chaitanya S.

APPLICANT: Mandbb, Andria

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND INSERVENCER

FILE REFERENCE: 210121,478C20

CURRENT FILING DATE: 2002-10-28

NUMBER OF SEQ ID NOS: 2157

SOFTWARE FEALES FEALES FOR Windows Version 4.0

SEQ ID NO 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          822
30
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
Score:
Percent Similarity:
100.00$
Best Local Similarity:
100.00$
Cuery Match:
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CONGANISM: Homo sapiens
US-10-283-017-1862
```

857 0000 0000 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: Score:
Score:
1.09e-15
Score:
Percent Similarity:
100.00\$
Best Local Similarity:
100.00\$
Dery Match:
100.00\$

20

22 ACGGCGCGTCCCGATACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC 81 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGl: ~ lyGlnGlyPheAlalleProlle

21 GlyGlnalaMetAlaileAlaGlyGlnile 30

US-09-684-215B-17 (1-30) x US-10-283-017-1862 (1-822)

ò

ò

US-09-684-215B-17 (1-30) x US-10-113-872-1862 (1-822)

22 ACGGCCCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCCGATC 81 1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle RESULT 27

Soquence 1877, Application US/09902941

Sequence 1877, Application US/09902941

Patent No. US20020172952A1

GENERAL INPORMATION:

APPLICANT: Henderson, Robert A.

APPLICANT: Wang, Tongtong ò

RESULT 25

US-10-017-754-1862
US-10-017-754-1862
Sequence 1862, Application US/10017754
Publication No. US20030054363A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Marnerakis, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Banger, Gary R.
APPLICANT: Banger, Gary R.
APPLICANT: Banger, Chaitanya S.
APPLICANT: Monabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TILE REFERENCE: 210121.478G18
CURRENT FILING DATE: 2001-10-29
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SSEQ ID NO 1862

```
US-09-684-215B-17 (1-30) x US-09-849-626-1877 (1-861)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.15e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Homo sapiens
US-10-283-017-1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 30
US-10-017-754-1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 ACGGCCCCCCCCATAACTTCCCAGCTGTCCCAGGGTGGCCAGGAATTCCCCATTCCCATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1877, Application US/09849626

Sequence 1877, Application No. US20020197669A1

GENERAL INFORMATION:
APPLICANT: Bangur. Chaitanya
APPLICANT: Fanger. Gary
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Switzer, Anne
APPLICANT: Clapper. Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C16
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT PILLING DATE: 2001.05-03
NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1877
LENGTH: 861
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Achter, Marc M.
APPLICANT: Retter, Marc M.
APPLICANT: Rancer, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Worklab, ComPositions AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILLE REFERENCE: 210121.478611
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2001
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1877
THORS OF THE CARTEN AND METHODS FOR THE THERAPY
CURRENT FILING DATE: 2001-07-10
CURRENT FILING BATE: 2002
CURRENT FILING BATE: 2001-07-10
CURRENT FILING BATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
0
0
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    861
30
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-215B-17 (1-30) x US-09-902-941-1877 (1-861)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.15e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
Score:
1.15e-15
Score:
148.00
Percent Similarity:
100.00$
Query Match:
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CRGANISM: Homo sapiens
US-09-849-626-1877
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Homo sapiens
US-09-902-941-1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 28
US-09-849-626-1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \delta
```

2 00.40.02 400

топ пау

```
ThralaalaserAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle 20
                                   22 ACGGCCGCGTCCGATAACTTCCAGCTCTCCCAGGGTGGGCAGCGATTCGCCATTCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProI
                                                                                                                                                                                                                 RESULT 29
US-10-283-017-1877
| Sequence 1877, Application US/10283017
| Sequence 1877, Application US/10283017
| Sequence 1877, Application US/10283017
| Publication No. US20030211510A1
| GENERAL INFORMATION:
| APPLICANT: Henderson, Robert A. APPLICANT: Aleah, Michael D. APPLICANT: Kalos, Michael D. APPLICANT: Glach, Paul R. APPLICANT: Johnson, Jeffrey C. APPLICANT: Garter, Marca W. APPLICANT: Garter, Darrick W. APPLICANT: Garter, Darrick C. APPLICANT: Danger, Gary R. APPLICANT: Banger, Chaitanya S. APPLICANT: Banger, Chaitanya S. APPLICANT: Morbb, Andria C. APPLICANT: Banger, C. COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER TITLE OF INVENTION: OWNOSITIONS AND DIAGNOSIS OF LUNG CANCER TITLE OF INVENTION: NUMBER: US/10/283,017
| CURRENT FILING DATE: 2002-10-28 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               861
30
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-684-215B-17 (1-30) x US-10-283-017-1877 (1-861)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 dedetadecearedecearedecedere 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                            82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                          21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1877, Application US/1001754
Publication No. US20030054363A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Waranabe, Yoshihiro
APPLICANT: Waranabe, Yoshihiro
APPLICANT: Waranabe, Jeffrey C.
APPLICANT: Marenabe, Marc W.
APPLICANT: Carter, Marc W.
APPLICANT: Arenerakis, Margarita
APPLICANT: Carter, Carter, Parrick
APPLICANT: Carter, Darrick
APPLICANT: Varter, Carter, Parrick
APPLICANT: Vardvick, Thomas S.
```

```
HAPLICANT: Bangur, Chaitanya S.
HAPLICANT: McMabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121-478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SEQ ID NO 1877
LENGTH: 861
LENGTH: 861
TYPE: DNA
ORGANISM: Homo sapiens
US-10-017-754-1877
                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Gaps:
                                                                                                                                                                                                                                                                                                 1.15e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Dest Match:
```

g ò

US-09-684-215B-17 (1-30) x US-10-017-754-1877 (1-861)

ò

Search completed: April 30, 2004, 05:10:22 Job time : 111.202 secs

protein

₹

Run on:

Sequence:

```
Mon May
```

```
Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
                                                                                                                                                                                                            Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                  Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                        Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                     Sequence
                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHODS FOR IMMUNOTHERAPY
OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE READABLE FORM:
MEDIUM TYPE RIOPY disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
GURRENT APPLICATION DATE:
FILING DATE: 13-MAR-1997
CLASSIFICATION: 42-47
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Steiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Wardzik, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Daniel R.
APPLICANT: OF INVENTION: CONFOUNDS AND METHODS FOR IMMUNC
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
US-09-685-166A-834
US-09-736-457-1861
US-09-606-421B-351
US-09-606-421B-351
US-09-606-421B-351
US-09-606-421B-351
US-09-606-421B-351
US-09-606-41B-351
US-09-620-412C-348
US-09-598-419-334
US-09-598-419-335
US-09-598-419-335
US-09-598-419-336
US-09-598-419-334
US-09-598-419-324
US-09-598-419-324
US-09-598-419-336
                                                                                                                                                                                                                                                                                                                                                     US-09-620-412C-356
                                                                                                                                                                                                                                                                                                                                                               US-09-598-419-356
US-09-620-412C-312
                                                                                                                                                                                                                                                                                                                                           US-09-598-419-340
                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-818-112-4
; Sequence 4, Application US/08818112
  Washington
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6290969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washingt
COUNTRY: USA
  Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 822, Appl
Sequence 822, Appl
Sequence 27, Appl
Sequence 352, Appl
Sequence 353, Appl
                                                                              April 29, 2004, 22:28:57; Search time 15:3589 Seconds (without alignments) 1083.969 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lssued_Patents_NA:*
11. /Ggn2_6/ptodatcy2/ina/5A_COMB.seq:*
12. /Ggn2_6/ptodatca/2/ina/5B_COMB.seq:*
31. /Ggn2_6/ptodatca/2/ina/6B_COMB.seq:*
41. /Ggn2_6/ptodatca/2/ina/6B_COMB.seq:*
42. /Ggn2_6/ptodatca/2/ina/PCTUS_COMB.seq:*
63. /Ggn2_6/ptodatca/2/ina/PCTUS_COMB.seq:*
64. /Ggn2_6/ptodatca/2/ina/PCTUS_COMB.seq:*
65. /Ggn2_6/ptodatca/2/ina/PcTUS_COMB.seq:*
66. /Ggn2_6/ptodatca/2/ina/PcTUS_COMB.seq:*
             GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                         nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-818-112-4
US-09-05-55-56-4
US-09-072-596-4
US-09-072-596-4
US-09-636-215-822
US-09-685-166A-822
US-09-685-166A-822
US-09-685-166A-822
US-09-736-457-1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-643-597-353
US-09-606-421B-353
US-09-636-215-834
                                                                                                                                          148
1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQI 30
                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                 682709 segs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                          BLOSUM62
Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0 Maximum DB seq length: 20000000000
                                                                                                                                US-09-684-215B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4444
4444
7444
675
675
825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                             Scoring table:
```

Database :

Result No.

```
1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                   ACGGCCGCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                        11 Acadecideciteccanhactriceachigicechagaideachaganteachartecannecane
                                                                                                                                                                                                1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44
00000
7
                   447
000
000
                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-684-215B-17 (1-30) x US-09-056-556-4 (1-447)
                                                                                                                                                          US-09-684-215B-17 (1-30) x US-08-818-111-4 (1-447)
                                                                                                                                                                                                                                                                                                                  71 GGCCAGGCGATGGCGATCGCGGGCCAGATC 100
                                                                                                                                                                                                                                                                              21 GlyGlnAlaMetAlaileAlaGlyGlnile 30
                   5.52e-16
148.00
100.00$
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.52e-16
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                    Percent Similarity:
Best Local Similarity:
Query Match:
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                         11 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGATC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Sekiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TOWNERS OF SEQUENCES: 148
COMPUTES: SEED and BERRY LLP
STREET: G300 Columbia Center, 701 Fifth Avenue
CITY: Seatile
COUNTRY: USA
ZIP: 93104-7092
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PRECEDION DATA:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: US-008/MS-DOS.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: US-008/MS-DOS.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REPRENCE/DOCKET NUMBER: 31,392
RESERVENCE/DOCKET NUMBER: 31,392
REPRENCE/DOCKET NUMBER: 31,392
REPRENCE/
                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                          US-09-684-215B-17 (1-30) x US-08-818-112-4 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08818111 Patent No. 6338852 GENERAL INFORMATION:
  (206) 622-4900
              TELEFAX: (206) 682-6931
| INFORMATION FOR SEQ ID NO: 4:
| SEQUENCE CHARACTERISTICS:
| LENOTH: 447 base pairs
| TYPE: nucleic acid
| STRANDENESS: single
| TOPOLOGY: linear
                                                                                                                                                                                                               5.52e-16
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-818-111-4
                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

TREAT

```
; Sequence 822, Application US/09636215; Patent No. 6620922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.52e-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-636-215-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-072-967-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ThralaalaseraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGCCAGGGATTCGCCATTCCGATC 70
                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven G.
APPLICANT: Reed, Yasir A.W.
APPLICANT: Dillon Davin C.
APPLICANT: Campos Neto, Antonia
APPLICANT: Campos Neto, Antonia
APPLICANT: Used C. Michael J.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: Galo Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY WEALINGTON

COUNTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

APPLICATION:

NAME: Maki, David J.

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 31,392

RELECOMMUTCATION INFORMATION:

TELEPHONE: (206) 682-6031

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTER.STICS:

LINFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTER.STICS:

LENGTH: 447 base pairs

TYPE: MUCLEL CALL

TYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-17 (1-30) x US-09-072-596-4 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 GGGCAGGCGATGGCGATCGCGGGCCAGATC 100
                                                           71 GGGCAGGCGATGGCGATCGCGGGCCAGATC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                          Sequence 4, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-072-967-4
; Sequence 4, Application US/09072967
; Patent No. 6592877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.52e-16
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-072-596-4
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
ò
```

```
1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Ramond
APPLICANT: Houghton, Ramond
APPLICANT: Vedvick, Taymond
APPLICANT: Vedvick, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendricken, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seartle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 Acescececteceanaacriceaerereceaecreseresereseareceear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/072,967

FILING DATE: 05-MAY-1998

CLASSIFICATION:

ATTORNEY AGENT INFORMATION:

NAME: Maki, David J.

REFERENCE/DOCKET NUMBER: 210121.411C9

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 447 base pairs

TYPE: muclaic acid

TYPE: muclaic acid

TYPE: muclaic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-17 (1-30) x US-09-072-967-4 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
```

```
US-09-684-215B-17 (1-30) x US-09-685-166A-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                              82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                        21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/09287849 Patent No. 6627198 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.75e-16
148.00
                                                                                      9.28e-16
148.00
100.00%
100.00%
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-822
                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
Score:
                                                                        Alignment Scores:
Pred. No.:
                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProlle 20
                                                                                                    APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: L1, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Skeiky, "Jasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITION OF PROSTATE CANCER
TITLE PREFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 Aceeccecercearaacriccaecreccaeeereeecaeearreecarr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      675
30
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-17 (1-30) x US-09-636-215-822 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 822, Application US/09685166A
Patent No. 6630305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.28e-16
148.00
100.00%
100.00%
  Kalos, Michael D
                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-09-636-215-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-685-166A-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
APPLICANT: SKENKY, Yadir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Marconio
APPLICANT: Corixa Corporation
ITILE OF INVENTION: and Their Uses
ITILE OF INVENTION: and Their Uses
ITILE PRICERENCE: 014056-009020US
CURRENT APPLICATION NUMBER: US 08/818,112
PRIOR APPLICANTION NUMBER: US 08/818,112
PRIOR PLING DATE: 1997-10-01
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1997-10-01
PRIOR PLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 AcGGCGGCGCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PENTURE: PEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     702
675
30
0
0
0
Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
```

```
1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 AcescececercearaActrecascrerceasesresseasesarrescentreseare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                           APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF THE OFFICE CANCER
TITLE OFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-06-421B-35-3

INS-08-421B-35-3

Patent No. 6531315

GENERAL INFORMATION:

APPLICANT: Wand, Tongtong

APPLICANT: Fan, Liqun

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Fanger, Cary R.

APPLICANT: Fanger, Cary R.

APPLICANT: Mang, Aijun

APPLICANT: Marg, Ailun

APPLICANT: Skeiky, Yasir A.W.

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: COMPOSITIONS

CURRENT PAPLICATION NUMBER: US/09/606,421B

CURRENT PAPLICATION NUMBER: US/09/606,421B

CURRENT PAPLICATION NUMBER: 2000-06-28

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSEQ for Windows Version 3.0

SSOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-684-215B-17 (1-30) x US-09-606-421B-353 (1-900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-684-215B-17 (1-30) x US-09-643-597-353 (1-900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 decrescionardecianicadescentare 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.33e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.33e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CRGANISM: Homo sapiens
US-09-643-597-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity: 1
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-606-421B-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-606-421B-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleFroIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                          25 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGTGGGGCAGGGATTCGCCATTCCGATC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1862, Application US/09736457

Patent No. 6509448

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Warter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Wang, Aljun
FILE REFERENCE: 210121.478615
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOCTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1862
LENGHH: 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
0
0
0
0
0
0
            0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-17 (1-30) x US-09-736-457-1862 (1-822)
                                                                                                                                                   US-09-684-215B-17 (1-30) x US-09-287-849-27 (1-702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 GGGCAGGCGATGCGGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                     21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 353, Application US/09643597; Patent No. 6426072; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang, Tongtong
Fan, Lidyn
Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148.00
100.00%
100.00%
      100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
US-09-736-457-1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-736-457-1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-09-643-597-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                            ò
```

```
ACGCCCCGTCCCGATAACTTCCAGCTCTCCCAGGGTGGCAGGGATTCCCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Weng, Aijun
APPLICANT: Weng, Aijun
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSITE CANCER
FILE REFERENCE: 20121.42.1701.7
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT APPLICATION NUMBER: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 834
LENGTH: 915
                                                                                                                                              82 édecadecearidecearicecedeceaere 111
                                                                                         21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                           RESULT 12
US-09-636-215-834
Sequence 834, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Nu'diangchun
APPLICANT: Mitcham, Davin C.
APPLICANT: Mitcham, Gennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Robert A.
APPLICANT: Headerson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Relos, Michael D.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Donn A.
APPLICANT: Carter, Donnas S.
APPLICANT: Li, Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-09-636-215-834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                                      22
                                                                                      ò
                                                                                                                                              g
```

APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT APPLICATION NUMBER: US/09/685,166A
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastESEQ for Windows Version 3.0
SEQ ID NO 834
LENGTH: 915

Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel

Retter, Marc W.

21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30 TYPE: DNA
CRGANISM: Homo sapiens
US-09-736-457-1861

21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30

Dp ò

US-09-684-215B-17 (1-30) x US-09-636-215-834 (1-915)

915 0 0 0 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

1.36e-15 148.00 100.00% 100.00%

Percent Similarity: Best Local Similarity: Query Match: DB:

Score:

Length: Matches: Conservative: Mismatches:

1.42e-15 148.00 100.00% 100.00%

Score: Percent Similarity: Best Local Similarity:

Alignment Scores: Pred. No.:

Sequence 834, Application US/09685166A
Sequence 834, Application US/09685166A
Septeman No. 6630305
Septeman Information
APPLICANT: Mitcham, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Mitchael D.
APPLICANT: Fanger, Gary R.

22 Accecceceteccanaacriccacrerccadgereceadgerecearcecarrecearc

US-09-684-215B-17 (1-30) x US-09-685-166A-834 (1-915)

915 00 00 00

Length:
Matches:
Conservative:
Mismatches:
Indels:

1.36e-15 148.00 100.00% 100.00%

Percent Similarity: Best Local Similarity: Query Match: DB:

TYPE: DNA
CORGANISM: Homo sapiens
US-09-685-166A-834

Alignment Scores: Pred. No.:

ò

d

ð

```
1.55e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.92e-15
148.00
100.00%
100.00%
                                                                                                             TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-421B-351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-636-215-851
                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                Query Match:
DB:
                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1012
30
0
0
0
  00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                               US-09-684-215B-17 (1-30) x US-09-736-457-1861 (1-945)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-17 (1-30) x US-09-643-597-351 (1-1012)
                                                                                                                     82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 GGGCAGGCGATGGCGATCGCGGGCCAGATC 156
                                                                                                21 GlyGlnAlaMetAlaileAlaGlyGlnile 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 16

US-09-606-421B-351
; Sequence 351, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Ralos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Panger, Chaitanya S.
; APPLICANT: Fanger, Gary
; APPLICANT: Li, Samuel X.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
                                                                                                                                                         US-09-643-597-351
; Sequence 351, Application US/09643597
; Patent No. 6426072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.55e-15
148.00
100.00%
100.00%
 100.001
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
DB:
```

à g

```
67 ACGGCCGCTCCGATAACTTCCAGCTGTCCCAGGGTGGGGCAGGATTCGCCATTCCGATC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProlle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-636-215-851
Sequence 851, Application US/09636215
Patent No. 6620923
GENERAL INFORMATION:
APPLICANT: Nu, Jiangchun C,
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Retter, Marc M.
APPLICANT: Retter, Marc M.
APPLICANT: Carter, John A.
APPLICANT: Oarle M.
APPLICANT: Oakle M.
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Mang, Aijun
APPLICANT: By Asir Milliam
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITION NUMBER: US/09/636,215
CURRENT FILICATION NUMBER: US/09/636,215
CURRENT FILICA DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 851
SEQ ID NO 858
SEG ID NO 858
SEG ID NO 858
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: ADD DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION WUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: SELSEEQ for Windows Version 3.0
SEQ ID NO 351
LENGTH: 1012
                                                                                                                                                                                                                                                                                                                                                                     1012
30
0
0
                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-17 (1-30) x US-09-606-421B-351 (1-1012)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
```

```
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 21
US-09-620-412C-332
                                                                                                                                                                  US-09-620-412C-348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-598-419-348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                       Query Match:
DB:
                                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThralaalaseraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 Acescecececerecentalerrecaserereceaseseseseseseseseseseseses 81
                                                                        20
                                                                                                        22 ACGCCCCCTCCCATAACTTCCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGATC 81
                                                                          ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Helple, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42721
CURRENT APPLICATION WHERE: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 851
LENGTH: 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 19
US-09-620-412C-148
US-09-620412C
; Sequence 348, Application US/09620412C
; Patent No. 6446234
; GENERAL INFORMATION:
; APPLICANT: SLEWYEN P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1203
30
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-684-215B-17 (1-30) x US-09-685-166A-851 (1-1203)
                                 US-09-684-215B-17 (1-30) x US-09-636-215-851 (1-1203)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 GGGCAGGCGATGGCGATCGCGGGGCCAGATC 111
                                                                                                                                                                                         82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                     21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                  Sequence 851, Application US/09685166A
parent No. 6630305
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Henderson, Robert A. APPLICANT: Ralos, Mitchael D. APPLICANT: Rater, Marc W. APPLICANT: Reter, Marc W. APPLICANT: Stolk, John A. APPLICANT: Stolk, John A. APPLICANT: Usefick, Thomas S. APPLICANT: Carter, Darrick APPLICANT: Li Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CONGANISM: Homo sapiens
US-09-685-166A-851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                RESULT 18
US-09-685-166A-851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                        d
                                                                                                                                                     ò
                                                                          ò
```

```
1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 Acedocercosanaacricoaerercocaeseresecaesearroscarrosearo
                                                                                                                                                                                                                                                                                                                                                                              1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 348, Application US/09598419
Facent No. 6565856
GENERAL INFORMATION:
FAPLICANT: Scheller, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREAIMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPRENCE: 210121.469066
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
SOFTWARE: PESESO ID NOS: 357
SOFTWARE: PESESO for Windows Version 3.0/4.0
SEQ ID NO 348
LENGTH: 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1464
330
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                          US-09-684-215B-17 (1-30) x US-09-620-412C-348 (1-1464)
                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-684-215B-17 (1-30) x US-09-598-419-348 (1-1464)
FILE REPERBNCE: 210121.469C7
CURRENT APPLICATION WINBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
LENGTH: 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GlyglnAlaMetAlaileAlaGlyGlnile 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 332, Application US/09620412C;
Patent No. 644824
GENERAL INFORMATION;
APPLICANT: Steven P. Fling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA; ORGANISM: Chlamydia trachomatis
US-09-598-419-348
                                                                                                                         TYPE: DNA ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.47e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                               2.47e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
```

```
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 Aceeccecercearaactrocaecrerceaesereeseaeseaeseaesearroscarrocarc 81
                                                                                                                                                                                                                                                                                                                                                                                                     1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                   22 Aceccecerceentacirceaeciereceaegraecaegaearregearregeare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 22
US-09-598-419-332
| Sequence 332, Application US/09598419
| Sequence 332, Application US/09598419
| Parent No. 6565856
| GENERAL INFORMATION:
| APPLICANT: Scholler, John N. APPLICANT: Scholler, John N. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT ITLE OF INVENTION: DAGNOSIS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121.469C6
| CURRENT APPLICANTION NUMBER: US/09/598,419
| CURRENT FILING DATE: 2000-06-20
| NUMBER OF SEQ ID NOS: 357-66-20
| SEQ ID NO 332
| SEQ ID NO 332
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REPERENCE: 210.12.146.97
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER: OF SEQ ID NOS: 363
SOFTWARE: FASELSEQ for Windows Version 3.0/4.0
SEQ ID NO 33.2
LENGTH: 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1557
30
0
0
0
0
                                                                                                                                                                                                                                               1557
30
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                             Length:
Matches:
Conservative: (
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-17 (1-30) x US-09-620-412C-332 (1-1557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-17 (1-30) x US-09-598-419-332 (1-1557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 edecadeceardecearcecedeceaearc 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 23
US-09-556-877-188
; Sequence 188, Application US/09556877
; Patent No. 6432916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CRGANISM: Chlymadia trachomatis
US-09-598-419-332
                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Chlymadia trachomatis
US-09-620-412C-332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.67e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                               2.67e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

```
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ACGGCCGCGTCCCATACTTCCAGCTGTCCCAGGGTGGCAGGGATTCGCCATTCCCATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 ACGGCCGCGCTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
GENERAL INFORMATION:
APPLICANT: Bratia, Ajay
APPLICANT: Bratia, Ajay
APPLICANT: Bratia, Ajay
APPLICANT: Steve
APPLICANT: Riing, Steve
APPLICANT: Maisonneuve, Jeff
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE REFERENCE: 210121,46595,877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 188
LENGTH: 1578
TYPE: DNA

COGANISM: Chlamydia

US-09-556-877-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 24
US-09-620-412C-188
US-09-620-412C-188
Sequence 188, Application US/09620412C
Ferent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.4697.
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 188
LUNCTH: 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1578
30
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                  1578
30
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-684-215B-17 (1-30) x US-09-620-412C-188 (1-1578)
                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-17 (1-30) x US-09-556-877-188 (1-1578)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 GGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GlyGlnAlaMetAlaileAlaGlyGlnile 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.710-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.: 2.71e-15
Score: 148.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Chlamydia
US-09-620-412C-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
DB:
```

```
82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ThralaalaserAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 ACGGCCGCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTGGCCATTCGATTC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGTGGGGCAGGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 26
US-09-620-412C-352

Sequence 352, Application US/09620412C

Sequence 352, Application US/09620412C

Sequence 352, Application US/09620412C

GENERAL INFORMATION:

APPLICANT Steven P. Fling

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

FILLS REPRENCE: 21021-465C7

CURRENT APPLICATION NUMBER: US/09/620,412C

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363

SOFTWARE: FestSEQ for Windows Version 3.0/4.0

SEQ ID NO 352

LENGTH: 1752
                  RESULT 25
US-09-598-419-188
is Sequence 188, Application US/09598419
Factor No. 6565856
GENERAL INFORMATION:
APPLICANT: SKelky, Yasir A.W.
APPLICANT: SKelky, Youn
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
FILE REPRENCE: 210.121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 188
: LENGTH: 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1752
30
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                               1578
30
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-684-215B-17 (1-30) x US-09-620-412C-352 (1-1752)
                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-17 (1-30) x US-09-598-419-188 (1-1578)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 GGCAGGCGATGCCGATCGCGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.09e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                             2.71e-15
148.00
100.00$
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OKGANISM: CDIA
US-09-620-412C-352
                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 28
US-09-20-412C-336
US-09-50-412C-336
Sequence 336, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
TITLE OF INVENTION: Pling
TITLE OF INVENTION: DAGNOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DAGNOSIS OF CHLAMYDIAL INFECTION
CURRENT APPLICATION NUMBER: US/09/620, 412C
CURRENT PILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOTTWARE: FREESEQ for Windows Version 3.0/4.0
SEQ ID NO 336
INFE: DAGNOSISM: Chlymadia trachomatis
US-09-620-412C-336
RESULT 27
US-09-598-419-352
US-09-598-419-352
Sequence 352, Application US/09598419
Sequence 352, Application US/09598419
Sequence 352, Application US/09598419
Sequence 352, Application US/09598419
Sequence 356, Search Control Compounds Applicant: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 352
LENGTH: 1752
TURE: DNA
CRAMISM: Chlamydia trachomatis
US-09-598-419-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1758
30
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                    1752
30
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-17 (1-30) x US-09-620-412C-336 (1-1758)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-684-215B-17 (1-30) x US-09-598-419-352 (1-1752)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.116-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                          3.09e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ACGGCCGCCCCATAAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 30
US-09-620-412C-308
is Sequence 308, Application US/09620412C
is Patent No. 6446234
is GENERAL INFORMATION:
APPLICANT: Steven P. Fling
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
ITILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
is SOFTWARE: FastsEQ for Windows Version 3.0/4.0
is LENGTH: 1860
                                                                                                Sequence 336, Application US/09598419

Sequence 336, Application US/09598419

Patent No. 6656856

GENERAL INFORMATION:

APPLICANT: Scholler, John

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

FILE REFERENCE: 210121.469C6

CURRENT FILING DATE: 2000-06-20

CURRENT FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 357

SOFTWARE: FastSEQ for Windows Version 3.0/4.0

SEQ ID NO 336

LENGTH: 1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-684-215B-17 (1-30) x US-09-620-412C-308 (1-1860)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-17 (1-30) x US-09-598-419-336 (1-1758)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-308
                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Chlymadia trachomatis
US-09-598-419-336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.346-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.116-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                       RESULT 29
US-09-598-419-336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
  ₽
```

1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20

```
22 ACGGCCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                    82 GGGCAGGCGATGCGCGGCCAGATC 111
                                                                   21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                            Search completed: April 30, 2004, 05:01:08 Job time : 17.3589 secs
                            g
```

```
/ Mon May 3 06:28:02 2004
```

U8-U9-684-715D-1/.rge

```
RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                April 29, 2004, 20:32:52 ; Search time 860.167 Seconds (without alignments) 1511.672 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6940544
GenCore version 5.1.ö
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                       OM protein - nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                US-09-684-215B-17
148
1 TAASDNPQLSQGGQGPAIPIGQAMAIAGQI 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3470272 seqs, 21671516995 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                         Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 ba: *
90 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2465
                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
```

em_vi:*	em_htg_hum:*	em_htg_inv:*	em_htg_other:*		htg	em_htg_rod:*	htg	htg	8y:	em_htgo_hum:*	em htgo mus:*	em_htgo_other:*	
29:	30:	31:	32:	33:	34:	35:	36:	37:	38:	39:	40:	41:	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	
TARI	
Š	

ੰ। ਦਾ ਦਾ ਦਾ ਦਾ ਦਾ ਦਾ	000000	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		5916 5916 3309 3309 5330 5330	100222000	AX169169 Sequence AR169152 Sequence AR182442 Sequence AR194825 Sequence AR333097 Sequence AR353302 Sequence
4 4 4 4 4 4 4 4 4 4 4 4 4 4 6 8 8 8 8 8			νονουνυνουουο	AX429596 AX832881 BD0063285 BD006445 BD006445 BD0064285 BD065285 AX400535 AX261049 AX261049 AX261049 AX263747 AR27344	AX429596 AX832581 BD00645 BD0069285 BD205817 AR405802 AR405802 AX201049 AX201049 AX201049 AX201049 AX201049 AX201049 AX201049 AX201049 AX201049	
4444444444	0000000000		<i>•••••••••••••••••••••••••••••••••••••</i>	2016 2016 2016 2016 2016 2016 2016 2016	2000 2000 2000 2000 2000 2000 2000 200	Sequency Sequency Sequency Sequency Sequency Sequency Sequency Sequency Sequency
• 4• 4• 4• 4• 4• 4• 4• 4• 4• 4• 4• 4• 4•	000000000000000000000000000000000000000	11111111111111111111111111111111111111	νονονονονονονονο		AR277644 AR22069151 AR22069151 AR265958 AR365958 BRD74033 AR369165 AR36919	«««««««««««««««««««««««««««««««««««««

ALIGNMENTS

PAT 20-APR-2002

4X369169

REFERENCE AUTHORS

JOURNAL

TITLE

FEATURES

ORIGIN

```
1 (bases 1 to 447)
Red,S.G., Skeiky,Y.A.W., Dillon,D.C., Campos-Neto,A., Houghton,R.,
Red,S.G., S. and Wardzik,D.R.
Compounds and methods for diagnosis of tuberculosis
Patent: US 6338852-A 4 15-JAN-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.

1 (bases 1 to 447)
Reed,S.G., Skeiky,Y.A.W. and Dillon,D.C.
Remositions and methods for the prevention and treatment of tuberculosis infection
Patent: US 6350456-A 4 26-FEB-2002;
Location/Qualifiers
                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447
                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.0000
7400000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 GGGCAGGCGATGGCGATCGCGGGCCAGATC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .447
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                21 GlyGlnAlaMetAlaileAlaGlyGlnile 30
                                                                                                                                                                                                                                                                                                                                                                       1. .447
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AR194825 4 from patent US 6350456.
AR194825 1 GI:20244262
                                                                                                                                                               447 bp
Sequence 4 from patent US 6338852.
AR182442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-684-215B-17 (1-30) x AR182442 (1-447)
US-09-684-215B-17 (1-30) x AR169152 (1-447)
                                                                                                                                                                                                           AR182442.1 GI:20225649
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.18e-13
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                       Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                        Unknown.
Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                          RESULT 3
AR182442
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                            . No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
AR194825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                     ď
                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM Unknown.

Unclassified.

I (bases 1 to 447)

RS Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S. and Twardzik, D.R.

Compounds and methods for immunotherapy and diagnosis of tuberculosis and methods for immunotherapy and diagnosis of tuberculosis

NAL Patent: US 629089-A 4 18-SEP-2001;

ES 1. Gation/Qualifiers

1. Gation/Qualifiers

/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 17-DEC-2001
                PAT 16-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                             I
Mang, T., Watanabe, Y., Henderson, R.A., Johnson, J.C., Retter, M.W.,
Marnerakis, M., Carter, D., Fanger, G. R., Vedvick, T.S., Bangur, C.S.,
Monabb, A., Fanger, N., Switzer, A., Moneill, P.D. and Clapper, J.D.
Compositions and methods for the therapy and diagnosis of lung
cancer.
Patent: WO 0204514-A 1879 17-JAN-2002;
CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4447
30
00
00
                                                                                                                                                                                                                                                                                                                                                                        186
000
000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                AX369169 1879 from Patent WO0204514.
Sequence 1879 from Patent WO0204514.
AX369169
                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AR169152 447 bp. Sequence 4 from patent US 6290969. AR169152. AR169152.1 GI:17906927
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215B-17 (1-30) x AX369169 (1-186)
                                                        AX369169.1 GI:18857178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.18e-13
148.00
100.00%
100.00%
100.00%
6
                                                                                                                                                                                                                                                                                                                                                                          4.60-14
148.00
100.00%
100.00%
                                                                                      Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
AR169152
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
               LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
```

ò g

à

PAT 20-APR-2002

REFERENCE AUTHORS

TITLE

JOURNAL FEATURES

ORIGIN

Score:

```
Reed, S.G., Skeiky, Y.A., Dillon, D.C., Campos-Neto, A., Houghton, R.L., Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for immunotherapy and diagnosis of tuberculosis and methods for immunotherapy and diagnosis of tuberculosis and methods for immunotherapy and diagnosis of tuberculosis and methods for immunotherapy and diagnosis of compounds in immunotherapy and diagnosis of Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 21-JUN-2002
                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44
00
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                       71 GGGCAGGCGATGGCGATCGCGGGCCAGATC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

    .447
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AX832581 447 bp
Sequence 4 from Patent EP1347055
AX832581 AX832581.1 GI:39840631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX429596 4 from Patent EP1203817.
AX429596 AX429596.1 GI:21540845
          /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-684-215B-17 (1-30) x AX429596 (1-447)
                                                                                                                                                                                                                                                                                       US-09-684-215B-17 (1-30) x AR353302 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.18e-13
148.00
100.00%
100.00%
                                                                                                    1.18e-13
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified unidentified unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
unidentified
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                        Similarity:
                                                                                                                                       Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
AX429596
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
SOURCE
ORGANISM
                                                                                                                                                                                             Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
AX832581
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ठे
                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
Unclassified.
Unclassified.
1 (Bases 1 to 447)
1 (A47)
1 (A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The faster of the factor of the faster of th
                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 20-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear PAT 17-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
                                                                                                                                                                                             20
                                                                                                                                                                                                                           70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                             1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               744
00
00
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
        Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4 from patent US 6592877.
AR353302.1 GI:33759108
                                                                                                                                                                                                                                                                                                                                                                                                                                               AR233097 447 bp
Sequence 4 from patent US 6458366.
AR233097 GI:27275533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-684-215B-17 (1-30) x AR233097 (1-447)
                                                                                                                                          US-09-684-215B-17 (1-30) x AR194825 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.18e-13
148.00
100.00%
100.00%
          100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity: 1
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
AR353302
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
CEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
AR233097
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                               à
```

PAT 12-DEC-2003

```
1.18e-13
148.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
     Sest Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C12N5/10//
PC (C12N1)
CC Strand
CC Topolo
FH Key
FT Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NETO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                       Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                               RESULT 10
BD006445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PI RAYMOND HOUGHTON, THOMAS S VEDVICK, DANIEL R TWARDZIK, PI MICHAEL J LODES

PC C Strandedness: Single,

CC Topology: Linear;

FH Key

Location/Qualifiers

FT source

/ Organism=' Unidentified'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08/818111 PI
ANTONIO CAMPOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ACGCCCCCCCCCCATACTTCCACCTCCCACGCTCCCACGCATCCCCATTCCCATTCCCATTCCCATTCCCATTCCCATTCCCATTCCCATTCCCATTCCCATTCCCATTCCCATTCCCATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThralaalaSerAspaenPheGlnLeuSerGlnGlyGlyGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unclassified.

1 (bases 1 to 447)

Reed.S.G., Skeiky, Y.A.W., Dillon,D.C., Neto,A.C., Houghton,R., Vedvick,T.S., Twardzik,D.R. and Lodes,M.J.
Compounds and methods for diagnosis of Tuberculosis
Patent: JP 2001500383-A 4 16-JAN-2001;
                  Reed, S.G., Skeiky, Y.A., Campos-Neto, A., Houghton, R.L., Vedvick, T.S., Twardzik, D.R. and Dillon, D.C. Compounds for immuncherapy and diagnosis of tuberculosis Petern: EP 1347055-A 4 24-SEP-2003; CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OS Unidentified
PN JP 2001500383-A/4
PD 16-JAN-2001
PP 07-CT-1997 JP 1998518432
PR 11-OCT-1996 US 08/729622,13-MAR-1997 US
STEVEN G REED,YASIR A W SKEIKY,DAVIN C DILLON, PI
                                                                                                                                                                                                                                                                                                                                               446
0000
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism='Unidentified'
                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 GGGCAGGCGATGGCGATCGCGGGCCAGATC 100

    .447
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .447
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-17 (1-30) x AX832581 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BD006325.1 GI:18634696
JP 2001500383-A/4.
unidentified
unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.18e-13
148.00
100.00%
                                                                                                                                                                                                                                                                                                                                            1.186-13
148.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                          Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
BD006325
LOCTOS
ACCESSION
VERSION
VERSION
CETYWEDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                       Alignment S
Pred. No.:
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                FEATURES
                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
BD006445
Twberculosis and methods for immunotherapy and diagnosis of Twberculosis.

Twberculosis.

BD006445.1 GI:18634816
S DP 2001501832-A/4.

Unidentified
PN JP 2001501832-A/4
PARZIXIA.W., Dillon,D.C., Neto,A.C., Houghton,R.,
Vedvick,T.S., Twardzik,D.R. and Lodes,M.J.
COMPOUNDS and methods for immunotherapy and diagnosis of
PATEN-2001
DATEN-2001
PN JP 2001501832-A/4
PN JP 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PI RAYMOND HOUGHIUN, ARGUEST COLORES OF CLORES OF COLORES OF CORRIS/62, PC COLORIS/60, GOIN33/50, GOINAGE GOINAGE
                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 ACGGCCGCGTCCCATACTTCCAGCTCTCCCAGGGTGGGCAGGATTCCCCATTCCGATC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70
                                                                                                                                                                                                                                                                                                                                                                        1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AcGCCCCCCCCATAACTTCCAGCTGTCCCAGGGTGGCCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444
0 0
0 0
0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ce 1. .447 / Organism='Unidentified'
Location/Qualifiers
             000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .447
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                       (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strandedness: Single;
Topology: Linear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-684-215B-17 (1-30) x BD006445
                                                                                                                                                                                                                                                       US-09-684-215B-17 (1-30) x BD006325
```

Ь

BD069285 LOCUS DEFINITION

RESULT 11

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

```
LODES,
RONALD C HENDRICKSON
C12N15/09,C07H21/02,C07H21/04,C07K7/00,C07K14/35,C07K16/12, PC
C12N15/09,C07H21/02,C07H21/04,C07K7/00,C07K14/35,C07K16/12, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 29-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                            K17/00,
C07K19/00,C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/04,C12Q1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 675)
Mashiki, Z. and Harada, J.
Negative pressure control apparatus for engine mounted in vehicle
Patent: US 6321716-A 822 27-NOV-2001;
Location/Qualifiers
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynabacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases I to 447)
Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C. Compounds and methods for diagnosis of tuberculosis
Patent: JP 2002530050-A 4 17-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                          PC C07K19/00,C12N1/19,C12N1/138/00,A61K39/04,A61K39/395,A61K39/PC 68,
PC G01N33/569,G01N33/68//A61K38/00,A61K39/04,A61K39/395,A61K39/PC 395,A61P31/06,
PC 395,A61P31/06,
PC (C12N1/21,C12R1:19),C12N15/00,C12N5/00,A61K37/02 CC
PC (CTN1/21,C12R1:19),C12N15/00,C12N5/00,A61K37/02 CC
Compounds and methods for diagnosis of tuberculosis.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                              RAYMOND HOUGHTON, THOMAS S VEDVICK, DANIEL R TWARDZIK, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OS Mycobacterium tuberculosis
PN JP 2002530050-A/4
PP 17-SEP-2002
PF 17-FEB-1999 JP 2000532132
PR 18-FEB-1999 US 09/024753,05-MAY-1998 US 09/072596 is
STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS
NETO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism='Mycobacterium tuberculosis'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.447
/organism="Mycobacterium tuberculosis"
/mol_type="genomic_DNA"
/db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447
30
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AR261272 675 bp DNA Sequence 822 from patent US 6321716.
AR261272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-684-215B-17 (1-30) x BD205817 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AR261272.1 GI:28072035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.18e-13
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown.
                                                                                                                                                                                                                                                                                                                                                                                            C07K17/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .. og
                                                                    REFERENCE
AUTHORS
                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR261272
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 17-JUL-2003
                                                                                        PAT 27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70
                                                                                                                                                                                                                                                                                                                                                                        OS Unidentified
PN JP 2001517069-A/4
PN JP 2001517069-A/4
PD 02-CCT-2001
PF 30-AUC-1996 JP 1997511464
PR 01-SEP-1996 US 08/523436, 22-SEP-1995 US 08/533634 PR 22-MAR-1996 US 08/659633 PR 12-UNL-19996 US 08/680574, 05-UNN-1996 US 08/68963 PR PR 212-UNL-19996 US 08/680574, 05-UNN-1996 US 08/680574

STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ប្ជ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ы
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unidentified unidentified.

1 (bases 1 to 447)

Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.H. and Twardzik, D.R.
Compounds and methods for immunotherapy and diagnosis of Patent: JP 2001517069-A 4 02-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C12N1/21//A61K39/04, (C12N1/21, C12R1:19)
Strandedness: Single;
Topology: Linear;
Compounds and methods for immunotherapy and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TANNON HOUGHTON THOMAS H VEDVICK, DANIEL R TWARDZIK PC C12N15/31, C07K14/35, A61K38/16, C12N15/62, G01N33/569, C12Q1/68, C12N5/10, PC C12N1/21/A61K39/04, (C12N1/21, C12R1:19)
CC Strandedness: Single;
CC Topology: Linear;
CC Topology: Linear;
CC Compounds and methods for immunotherapy and diagnosis of
                                                                                                    Compounds and methods for immunotherapy and diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compounds and methods for diagnosis of tuberculosis.
BD205817.1 GI:33015587
JP 2002530050-B/4.
Mycobacterium tuberculosis
                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447
30
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ce 1. .447
/organism='Unidentified'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 GGGCAGGCGATGGCGATCGCGGGCCAGATC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                  GGGCAGGCGATGGCGATCGCGGGCCAGATC 100

    .447
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-17 (1-30) x BD069285 (1-447)
                                                                                            447 bp
                                                                                                                                                                 BD069285.1 GI:22614888
JP 2001517069-A/4.
unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.18e-13
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                            BD069285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
```

source

FEATURES

Pred. No.:

70

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 12 BD205817 LOCUS

g

ò g à

DRIGIN

원

g ð

```
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Sted,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J. Compositions and methods for the therapy and diagnosis of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGAATTCGCCATTCGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                               1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                             22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               675
000
000
000
                                                                                                                                                                                675
30
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: WO 0151633-A 679 19-JUL-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  AX201049 675 bp D Sequence 679 from Patent WO0151633. AX201049 AX201049.1 GI:15390857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .675
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                               21 GlyGlnAlaMetAlaileAlaGlyGlnile 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-684-215B-17 (1-30) x AX201049 (1-675)
                                                                                                                                                                                                                                                                       US-09-684-215B-17 (1-30) x AR405802 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
Score:
148.00
Percent Similarity:
100.00$
Query Match:
100.00$
                                                                                                                                                                            1.83e-13
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                 Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 16
AX201049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                              JOURNAL
      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                             FEATURES
                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                              DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                   ଟ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 18-DEC-2003
                                                                                                                                                                                                                                                                                      PAT 18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                           Unclassified.

1 (bases 1 to 675)

Xu, J. Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,

Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,

Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,

Kalos, M.T., and Henderson, R.A.,

Compositions and methods for the therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                            20
                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ThralahlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                           675
00
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  675
30
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer
Patent: US 6620922-A 822 16-SEP-2003;
Location/Qualifiers
1. 675
/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            675 bp DI
US 6630305.
                                                                                                                                                                                                                             GGGCAGGCGATGCCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                      AR400535
Sequence 822 from patent US 6620922.
AR400535
AR400535.1 GI:40144000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                           21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-684-215B-17 (1-30) x AR400535 (1-675)
                                                                                                                                   US-09-684-215B-17 (1-30) x AR261272 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AR405802
Sequence 822 from patent
AR405802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AR405802.1 GI:40154639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.83e-13
148.00
100.00%
100.00%
                                           1.83e-13
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown.
Unclassified.
1 (bases 1 to 6
                                                         Score:
Percent Similarity:
Dest Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unknown.
                                                                                                                                                                                                                                                                                                                                              .
Unknown.
                                                                                                                                                                                                                                                                                                                                                                  Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                   Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
AR405802
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                           RESULT 14
AR400535
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                 Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
```

ORIGIN

g ò

PAT 29-AUG-2001

20 81 딞

TITLE

```
PAT 18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unclassified.

1 (bases 1 to 702)
Reed,S.G., Skeiky,Y.A., Dillon,D.C., Alderson,M. and Campos-Neto,A. Fusion proteins of Mycobacterium tuberculosis antigens and their
                                   Mtb24), reading frame 1
bi-fusion protein Ral2-DPPD (designated Mtb24), reading frame reading frame 2
reading frame 3
Rey (1). (696)
CDS (1). (696)
CDS (2). (700)
CDS (3). (700)
                                                                                                                                                                                                                                                                                                                                                                                             CC Description of Artificial Sequence:bi-fusion protein Ral2-DPPD
CC Mtb24), reading frame 1
CC bi-fusion protein Ral2-DPPD (designated Mtb24), 1
CC reading frame 3
FH Key Loss (1). (596)
FT CDS (2). (700)
FT CDS (2). (700)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7000000
                                                                                                                                                                                                                                                                  30
30
0
0
0
                                                                                              Location/Qualifiers
(1) . (696)
(2) . (700)
S (2) . (701)
Location/Qualifiers
1. 702
1. 702
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent: US 6627198-A 27 30-SEP-2003;
Location/Qualifiers
Location/Qualifiers
/ r 702
/ organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR403747 702 bp C
Sequence 27 from patent US 6627198.
AR403747.1 GI:40151423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-17 (1-30) x BD251334 (1-702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-684-215B-17 (1-30) x AR403747 (1-702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.91e-13
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                    1.916-13
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 19
AR403747
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                     Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
FEATURES
                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BD251334.1 GI:33061104
BD251334.1 GI:33061104
JP 2002510494-A/13.
Synthetic construct
synthetic construct
artificial sequences.
1 (bases I to 702)
Skeiky, Y.A.W., Alderson, M. and Neto, A.C.
Fused protein of Mycobacterium tuberculosis antigen and utilization thereof
                                                                                                                                                                                  Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T. and Henderson,R.A. Compositions and methods for the therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BD251334 7052 bp DNA linear PAT 17-JUL-2003 Fused protein of Mycobacterium tuberculosis antigen and utilization thereof.
                                                            PAT 26-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OS Artificial Sequence
PN JP 2002510494-A/13
PD 09-ARR-2002
PD 09-ARR-1999 US 09/056556,30-DEC-1998 US 09/223040 PI
YASIR A W SKEIKY, MARK ALDERSCN, ANTONIO CAMPOS NETO PC
C12N15/09,A61K39/04,A61K48/00,A61P31/04,C07K14/35,C07K19/00, PC
PC C12N15/00
                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                         675
30
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                 cancer.
Patent: WO 0173032-A 822 04-OCT-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
1. 675
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: JP 2002510494-A 13 09-AFR-2002;
CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111
                                                     Sequence 822 from Patent WO0173032.
AXX67848
AX267848.1 GI:16516494
     GGGCAGGCGATGGCGATCGCGGGCCAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-684-215B-17 (1-30) x AX267848 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                         1.83e-13
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity: 1
Best Local Similarity: 1:
Query Match: 1:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                             AZ267848
LOCUS
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWOLDS
SOUNCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 18
BD251334
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                  JOURNAL
```

d

8 g à 20 84

COMMENT

Query Match: 100.00% Indels: 0	-684-215B-17 (1-30) x AX369152 (1-822) 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGll[rimates; Hendersc Switzer, lods for t 1877 17-4	FEATURES Continuation (19) Bource 1861 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Alignment Scores: 2.38e-13 Length: 861 Pred. No.: 2.38e-13 Length: 861 Score: 148.00 Matches: 30 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 DB: 6 Gaps: 0	Alaalaseraspasphed GCGGTCCGATACTTCC GLANIAMETAIAILEALAG GINALAMETAIAILEALAG CAGGCGATGGCGATCGCGG	RESULT 23 AX351489 LOCUS SA351489 LOCUS AX351489 LOCUS ACCESSION AX351489 AX351489 VERSION AX351489.1 GI:18616835 VERYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (hordata: Craniata: Vertebrata; Euteleostomi;	Prinates; Catarrhin; Hominidae; Homo Capper, J. D., Wang, A. and Secrist, hods for the therapy and diagnosis of 236 20-DEC-2001;
Db 85 GGGCAGGCGATGGCGAGCCAGATC 114	RESULT 20 AR277645 AR277645 AR277645 B822 bp DNA linear PAT 10-APR-2003 DEFINITION Sequence 1862 from patent US 6509448. ACCESSION AR277645 VERSION AR277645 Unknown. ORGANISM Unclassified. Unclassified. Unclassified. REFERENCE Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S., Carter, D., Retrer, M.W., Mannion, J., Fan, L. and Wang, A. TITLE Compositions and methods for the therapy and diagnosis of lung cancer JOURNAL Patent: US 6509448-A 1862 21-JAN-2003; FRATURES SOURCE // Organism="unknown" // Mol_type="genomic DNA"	Alignment Scores: 2.26e-13 Length: 822 Score: 148.00 Matches: 30 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 100.00\$ Indels: 0 DB:	-09-684-215B-17 (1-30) x AR277645 (1-822) 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGl	Qy 21 GlydlnAlaMetAlaIleAlaGlydlnIle 30 Db 82 GGGCAGGCGATGGCGGCCAGATC 111 RESULT 21 AX369152 LOCUS AX369152 DEFINITION Sequence 1862 from Patent W00204514. VPSGTON AX369152		Monabb, A., Fanger, N., Switzer, A., Moneill, P.D. and Clapper, J.D. TITLE Compositions and methods for the therapy and diagnosis of lung cancer JOURNAL Parent: WO 0204514A 1862 17-JAN-2002; CORIXA CORPORATION (US) FEATURES 1. 822 1. 822 1. 822 1. 624 Molitype="Homo Sapiens" /molitype="Homo Sapiens" /db_xref="taxon:9606"	Alignment Scores: 2.26e-13 Length: 822 Prod. No.: 148.00 Matches: 30 Score: 100.00\$ Conservative: 0 Bercent Similarity: 100.00\$ Mismatches 0

SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REPERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REPERENCE AUTHORS Wang, A., Skeiky, Y.A., Li,S.X., Kalos, M.D., Henderson, R.A., Mcneill, P.D., Fanger, N., Watanabe, Y. and Peckham, D.M. Vedvick, T.S., Catrer, D., Watanabe, Y. and Peckham, D.M. Compositions and methods for the therapy and diagnosis of lung ance JOURNAL Patent: WO 0200174-A 353 03-JAN-2002; FEATURES CORIA CORPACATION (US) FEATURES L. 900 // Mol_type="unassigned DNA" // Mol_type="una	(1-30) x AX365960 (1-900) AlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	AUTHORS
CORIXA CORPORATION (US) FOURES Location/Qualifiers 1. 894	24 90 FION NA NISM NISM NCE ORS E	Alignment Scores: Alignment Scores: Scores: 148.00 Matches: Scores: 148.00 Matches: Scores: 100.00\$ Masmatches: Conservative: Masmatches: Conservative: Best Local Similarity: 100.00\$ Masmatches: Gaps: Ouery Match: (1-30) A RA220690 (1-900) Qy 1 ThralablaSerAspasnPheGlnClwGerGlnGlyGheAlaileProile 20 ThralablaSerAspasnPheGlnClwGerGrGcGGGGGGGGGGGTGGGCGTTCGGTC Qy ThralablaSerAspasnPheGlnClwGerGrGcGGGGGGGGGGGTTCGCGTTCGGTC Qy ThralablaMetAlaileAlaGlyGlnIle 30

```
linear PAT 29-JAN-2003
                                                                                                                                                                                                                 yGlnGlyPhealalleProlle 20
                                                                                                                                 engine mounted in vehicle
                                       yGlnGlyPhealaileProile 20
                                                                                                                                                                          00000
```

RESULT 27
AR400544
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM

REFERENCE AUTHORS

source

ORIGIN

JOURNAL

TITLE

FEATURES

```
PAT 26-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu.J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
                                                                                                                                                                                                                                                                                                             Xu.J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J. Compositions and methods for the therapy and diagnosis of prostate cancer
                                                                                                                                                                                       PAT 29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                         Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                              Parent: WO 0151633-A 691 19-JUL-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AX267860 915 bp D
Sequence 834 from Patent WO0173032.
AX267860
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                      AX201061 915 bp D
Sequence 691 from Patent WO0151633.
AX201061
AX201061.1 GI:15390868
 Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-215B-17 (1-30) x AX201061 (1-915)
                                      US-09-684-215B-17 (1-30) x AR405811 (1-915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AX267860.1 GI:16516503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
Score:
148.00
Percent Similarity:
100.00$
Dest Local Similarity:
100.00$
Dest Match:
100.00$
                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
100.00%
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 30
AX267860
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
SOURCE
ORGANISM
                                                                                                                                                             RESULT 29
AX201061
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
SCYWORDS
SOURCE
ORGANISM
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                          Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                 В
                                                                                                               ઠે
                                                                                                                                       셤
                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 18-DEC-2003
                                                                                                                                       Unclassified.

(Dassal to 915)

Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,

Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,

Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,

Hepler, W.T. and Henderson, R.A.

Compositions and methods for the therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     915
30
0
                                                                                                                                                                                                                                                                                                                                              915
00
00
0
                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ON
                                                                                                                                                                                                                                         Patent: US 6620922-A 834 16-SEP-2003;
Location/Qualifiers
1. 915
/ organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR405811
Sequence 834 from patent US 663030S.
AR405811.
AR405811.1 GI:40154648
 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                  AR400544 915 bp D
Sequence 834 from patent US 6620922.
AR400544 AR400541. GI:40144016
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-684-215B-17 (1-30) x AR400544 (1-915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.54e-13
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                            2.54e-13
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
Unknown.
                                                                                                         unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown
                                                                                                                              Unknown
                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 28
AR405811
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
```

à Db ò 셤 20

REFERENCE AUTHORS

JOURNAL

TITLE

FEATURES

ORIGIN

Mon May

```
Compositions and methods for the therapy and diagnosis of prostate cancer
Patent: WO 0173032-A 834 04-OCT-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
1. 915
/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
                                                                             FEATURES
SOURCE
                                            JOURNAL
            TITLE
                                                                                                                                                                   ORIGIN
```

US-09-684-215B-17 (1-30) x AX267860 (1-915) Pred. No.: 2.54e-13 Score: 148.00 Percent Similarity: 100.00\$ Best Local Similarity: 100.00\$ Query Match: 100.00\$

Alignment Scores: Pred. No.:

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

21 GlyGlnalaMetalailealaGlyGlnile 30

> DP ò

à

Search completed: April 30, 2004, 02:24:01 Job time : 861.167 secs

29: gb gss2:*

```
ო
Mon May
 183
```

Run on:

```
CF619317 AGENCOURT
CF619317789 BB077789
CR930964 MTU2TA.P1
BIOTOS64 CO040P04U
BIOTOS64 CO040P04U
BIOTOS64 CO040P04U
BIOTOS64 CO040P04U
CA9311960 MTUGTA.P2
CA931208 MTUGTA.P2
CA931208 MTUGTA.P2
CA931308 MTUGTA.P2
CA933138 MTUGTA.P2
CA933138 MTUGTA.P2
CA933116 MTUGTR.P3
CA923116 MTUGTR.P3
CA923116 MTUGTR.P1
CA922028 MTUGTR.P1
CA922028 MTUGTR.P1
CA922028 MTUGTR.P1
CA927647 MTUGTR.P1
CA931105 MTUGTR.P1
CA931105 MTUGTR.P1
CA931105 MTUGTR.P1
CA931105 WTUGTR.P1
CA9280326 MTUGTR.P2
CA9311061 WA38BCO6
A11665 WTUGTR.P2
CA9311061 WA38BCO6
A1164854 A0699720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 03-APR-2003
                                                                                                        PtaC0016C
AGENCOURT
BB077789
PopSC0010
MTU2TA.P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BST.

Mus musculus (house mouse)

Mus musculus

Mus musculus

Mus musculus

Mamaria; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 747)
                                                                                             CB597827 AGENCOURT
CF231012 PtaC0016C
       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CBS97827
AGENCOURT 12972312 NIH_MGC_178 Mus musculus cDNA clone
IMAGE:30297156 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                               SUMMARIES
                                                                                            CR597827
CF6191012
CF6191012
CF6193014
CA930964
BIO70561
BIO70561
BIO70561
BIO70561
CA9311960
CA9311960
CA9321038
CA9321038
CA9321038
CA9321038
CA9321038
CA9321038
CA9321038
CA9321038
CA9321038
CA932104
CA9311169
CA9311169
CA931169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBS97827.1 GI:29515683
                                                                           B
                                                                                                                          Length
                                                                  Query
                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
CB597827/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                しょしょしょう ちゅうしゅう ちゅうしょう しゅうしょう しゅうしゅう
                                                                                                                                                                                                                                                                                                                                                                       υυυ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 0 0 0 0 0 0 0
                                                                                                                                                                                                                                      0000000
                                                                                                                                                                                                                                                                                                                             0000
                                                                                                                                                                            U
                                                                                              U
                                                                                                                                                                                                                                                                                                      Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q02EL=frame+ p2n.model -DEV=xlh
-Q2/cgn2 1/USPTO_spool/USC09684215/runat 29042004 061305 13200/app_query.fasta_111B0
-Q2/cgn2 1/USPTO_spool/USC09684215/runat 29042004 061305 13200/app_query.fasta_111B0
-Q2/cgn2 1/USPTO_spool/USC09684215/runat_200-1TRANS=human40.cdi -115T=45
-UNITS=b1ts -START=1 -RND=-1 -MATRIX=b100 -THR MINE 0 -ALIGN=30 -MODE=LOCAL
-OUTPMT=ptc -NORM=&Xt -HEAPSIZE=560 - MINE NINE 0 -MXLEN=2000000000
-USER=US09684215_@CGN 1 1 5167 @runat_29042004 061305 13200 -NCPU=6 -ICPU=3
-NOW MAAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DSV TIMBOUT=120 -WARN TIMBOUT=30 -THRANS=1 -XGAPOP=6 -DELEXT=7 -XGAPOP=10 -XGAPOP=6 -DELEXT=7
                                                       April 29, 2004, 22:25:27; Search. Jime 587.584 Seconds (without alignments) 1524.660 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                     nucleic search, using frame_plus_p2n model
                                                                                             US-09-684-215B-17
148
1 TAASDNPQLSQGGQGFAIPIGQAMAIAGQI 30
                                                                                                                                                                                               27513289 segs, 14931090276 residues
                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  BLOSUM62
Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_gss_mam: *
em_gss_mus: *
em_gss_pro: *
em_gss_rod: *
em_gss_vri: *
gb_gssl: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gss_hum:*
gss_inv:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gss vrt:*
gss fun:*
                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_gss_pln:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_estfun:*
                                                                                                                                                                                                                                                                                                                                                                                                                                     em_estba:*
em_estbum:;
em_estbum:;
em_estcov:;
em_estcov:;
em_btc:*
gb_est1:;
gb_est2:;
gb_est3:;
gb_est4:;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_estom:*
                                                                                                                                                                                                                                                                                                                                                                                                                             EST:*
                                                                                              Title:
Perfect score:
                                                                                                                                    Scoring table:
                                     OM protein
                                                                                                                  Sequence:
                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                             Database
```

```
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
CF619317/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
AL Unpublished (1999)

Outlact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov/.

Tissue Procurement: Dr. Michael Brownstein

CDNA Library Preparation: Michael Brownstein

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloosience Corporation

Clone distribution: MGC clone distribution information can be http://mage.llnl.gov

Plate: NDCM57 row: j column: 13

High quality sequence stop: 475.

High quality sequence stop: 475.

Accanism="Mus musculus"

/mol type="mRNA"

/mol type="mRNA"

/doc="mRNA"

/doc="mRNA"

/clone="mRNAE: 30297156"

/lab host="mRNAE: 30297156"

/lab host="mRNAE"

/clone="mRNAE"

/clone="mRNAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                620 bp mRNA linear BST 05-AUG-2003 PtaC0016C2C0206 Populus cDNA library from cambial zone Populus alba x Populus tremula cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Populus alba x Populus tremula
Populus alba x Populus tremula
Populus alba x Populus tremula
Bopulus alba x Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida I; Malpighiales; Salicaceae; Saliceae; Populus.

| (bases 1 to 620)
| (bases 1 to 620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed sequence tags from poplar tension wood tissues - A comparative analysis from multiple libraries Unpublished (2003) Contact: Leple JC Unit of Forest improvement, Genetics and Physiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-684-215B-17 (1-30) x CB597827 (1-747)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CF231012.1 GI:33450441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111
60.00
70.83%
54.17%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                575 GCGGGGCAGCTT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 AlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pilate, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
CF231012
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
           AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
```

```
/tissue_type="cambial zone harvested on the bark side"
/dev_stage="3-years-old poplar trees grown in the nursery"
/clone_lbe="poplar cDNA library from cambial zone"
/clone_lbe="poplar cDNA library from cambial zone"
/note="A composite cDNA library was made with mRNA
isolated from opposite and tension wood tissues
corresponding to the cambial zone collected on the bark
side after debarking the stem. In this respect, in
addition to cambium cDNA, this library also contains very
young phloem and very young xylem cDNA. The sampling was
done on 3 different tilted trees grown in the nursery.
CDNA were cloned in an oriented way into SfiI (A and B)
restriction sites. A one-step conversion of Lambda
Triplex2 to the corresponding priplex2 plasmid was done
via site-specific recombination at loxP sites (Clontech;
SMART CDNA library construction kit). CDNA inserts were
RCR amplificad using glanking primers and then sequenced on
a ABI3100 Genetic Analyser (Applied Biosystem)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF619317
AGENCOURT 15738624 NIH MGC 219 Homo sapiens cDNA clone IMAGE:30523641 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ThralaalaseraspasnPheGlnLeuserGlnGlyGlyGlnGlyPheAlalleProlle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 899)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIT Wasser 10 2007)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
National Institute for Agricultural Research (INRA)
Domains de Limere, BP20619 ARDON, 45166 OLIVET CEDEX, FRANCE
Tel: 33 02 38 41 78 09
Fax: 33 02 38 41 78 09
Email: Jean-Charles Leple@orleans.inra.fr
BCR PRIMERS
FOR PRIMERS
FORWARD: TriplexA 5' CTCGGGAAGCGCCCATTGTG 3'
BACKWARD: TriplexB 5' CTCGGGAAGCGCCCATTGTG 3'
BACKWARD: TriplexB 5' CTCGGGAAGCGCCCATTGTG 3'
Seq primer: TriplexB 5' CTCGGGAAGCGCCCATTGTG 3'
Seq primer: TriplexB 5' CTCGGGAAGCGCCCATTGTG 3'.
                                                                                                                                                                                                                                                                                                                                                   l. .620
organism="Populus alba x Populus tremula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00
8 <del>0</del> 10
00
8 <del>0</del> 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/grrain="cloom INRA 717-1-B4"
/db_xref="taxon:80863"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
National Cancer Institute / NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1-620)
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-684-215B-17 (1-30) x CF231012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF619317
CF619317.1 GI:37238006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||::: |||
321 GGAGAAGTGATG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
```

```
Email: genome-resegac riken.go.jp,

URL:http://genome-gac.riken.go.jp,
URL:http://genome-gac.riken.go.jp,
Carninol.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Okazaki,Y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M.,
System. Genome Res. 9 (5), 463-470 (1999)
Carninoi,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Sugahara,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
Takahashi,F., Tominaga,N., Towa,T., Tsunoda,Y., Wataniki,A.,
Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.
RIKBN Mouse ESTS (Konno,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
I-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="diencephalon"
/dev_stage="adult"
| Jab_host="DH10B"
/clone lib="RIKEN full-length enriched, adult male
diencephalon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="9330145E04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71
57.00
75.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                          TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                       /mol type="memory coeptions"
//mol type="memory coeptions"
/db_xref="raxon.9606"
/clone='IMAGE.302364"
/tlosue_type="Pooled Chondrosarcoma Tumor cells"
/lab_host="PubloB (T1 phage-resistant)"
/clonellab="Whith MGC_219"
/clonellab="Whith MGC_219"
/note="Wetcor: pX-Asc; Site_1: EcoRI; Site_2: NotI;
/note="Wetcor: pX-Asc; Site_1: EcoRI; Site_2: NotI;
/note="Wetcor: pX-Asc; Site_1: EcoRI; Site_2: NotI;
/inter containing a Not I site. Double strand cDNA was size primed and directionally into pX-Asc vector. Average insert size
0:5-IKA Adaptors S'(AATTGGGCAGAGG)? and S'd
(CTCGTGCCG)3: 3' Linker sequence - GCGGGCGCTAAAGGC TI8.
Sequencing primers 3'end: T3 promoter primer S'd
(ATTAACCTCTCAAAGGGA)3: 5' End: T7 promoter primer S'd
(TAATAACCTCTCAAAGGGA)3: 5' Library was constructed in the laboratory of M. Bento Soares. Average insert size 2-3kb.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 238)
Konno.H., Aizawa.K., Akahira,S., Akiyama,J., Arakawa,T.,
Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 27-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 bp mRNA linear EST 27-JUN-2000 BB077789 RIKEN full-length enriched, adult male diencephalon Mus Musculus CDNA clone 9330145E04 3' similar to AF178432 Homo sapiens BB077789 GI:8642849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   677 Accessornessracscricaactroicaassescescescescerectroce 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 238)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                          Email: cgapDS-remail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
thtp://image.lln.gov
Plate: NDAMGOI row: o column: 10
High quality sequence start: 55
High quality sequence stop: 553.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         899
111
0000
0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
          Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-17 (1-30) x CF619317 (1-899)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||::: :::|||:::
617 GGGAGGCCCTTGGCAGTA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlyGlnAlaMetAlaile 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281
58.00
61.54%
42.31%
39.19%
                                                                                                                                                                                                                                                                                                                                    .899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
BB077789/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                            FEATURES
```

ORIGIN

Score:

ò d ò

```
BI070561
C040P04U Populus strain T89 leaves Populus tremula x Populus
tremuloides CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Malpighiales; Salicaceae, Saliceae, Populus.
(bases 1 to 343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
        MTU2TA.P13.A01 Aspen apex cDNA Library Populus tremuloides cDNA,
                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2003)
Contact: Tsai C-J
Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Emx: 906 487 2914
Email: chtsai@mtu.edu.
                                                                                                                                                                                                                                                                                         Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and
Tsai, C-J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .343 | Corganism="Populus tremuloides" | /organism="Populus tremuloides" | /mol_type="mra.na." | /db xref="taxon:3693" | /clone lib="Aspen apex cDNA Library" | /note="Organ: apex" | /note="Organ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Biotechnology
Royal Institute of Technology
Frankrikzingen 30, Stockholm S-10044, Sweden
Tel: 46 8 790 8287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                    Populus tremuloides (quaking aspen)
Populus tremuloides
                                                                                                                                                                                                                                                                                                                                                 Expressed sequence tags from Aspen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-17 (1-30) x CA930964 (1-343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI070561
BI070561.1 GI:14491181
                                                       CA930964
CA930964.1 GI:27419444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Erlandsson R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1114
57.00
66.67%
41.67%
38.51%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||::: |||
258 GGAGAATGATG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMet 24
                                   mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
BI070561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Epulus alba x Populus glandulosa

Populus alba x Populus glandulosa

Populus alba x Populus glandulosa

Populus alba x Populus glandulosa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Malpighiales; Salicaee; Saliceae; Populus.

Ele.J.S., Lee.H.S., Noh,E.W. and Choi,Y.I.

Gene Expression Profiling of the Poplar Suspension Cell

Unpublished (2003)

Contact: Jae-Soon Lee

Biotechnology Team

Korea Forest Research Institute

44-3 Omockchun-dong, Suwon, 441-350, Korea

Fax: 82 31 290 1020

Email: jasolee@foa.go.kr
                                                                                                                                                                                                                                                                                       336 bp mRNA linear EST 03-FEB-2003
PopSC00108 Poplar SC cDNA library Populus alba x Populus glandulosa
CBDA clone PopSC00108, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 30-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 ACATCTGGAGCAGAGGAATTCGAAGGTGTCCAAGGAGGATCAGGGTTCGCATTTCTCGCA 302
                                                                                                                                                                                           9 LeuSerGlnGlyGlnGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGly 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProlle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Suspension cell"
/lab host="XII-Blue MRF" strain"
/clone lib="Poplar SC CBNA library"
/note="Vector: Uni-ZAP XR; Site_1: EcoRI; Site_2: Xho!"

    .336
    /organism="Populus alba x Populus glandulosa"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
        ω o o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
        Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert Length: 336 Std Error: 0.00 Seq primer: T3 POLYA=No.
                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:153471"
/clone="PopSC00108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-684-215B-17 (1-30) x CB184974 (1-336)
                                                                                                           US-09-684-215B-17 (1-30) x BB077789 (1-238)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      CB184974.1 GI:28196969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
57.00
66.67%
41.67%
38.51%
     45.00%
38.51%
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||::: |||
303 GGAGAAATGATG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: T3
BACKWARD: T7
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA930964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . No. :
                                                                                                                                                                                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                              RESULT 5
CB184974
                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
CA930964
LOCUS
```

FEATURES

ORIGIN

ò g

g 8

```
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 GCC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 Ala 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsai, C-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
DB:
                                                                                                                                                                                                                                                                                       Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
CA931030/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 366)
1 (Dases 1 to 366)
Dias Neto. E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunsein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3£t2=CM3-GN0330-
120201-735-e08£t3=2001-02-12£t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366 bp mRNA linear EST 15-JUN-2001 CM3-GN0330-120201-735-e08 GN0330 Homo sapiens cDNA, mRNA sequence. BI055877 BI055877 EST. GI:14463407 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                              1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 ACATCTGGAGGAGGAGTTCGAAGTGTTCCAAGGAGGATCAGGGTTCGCATTTCTCGCA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sao Paulo-SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
                                                         1. 351
/ Organism="Populus tremula x Populus tremuloides"
/ Organism="Populus tremula x Populus tremuloides"
/ Strain="T89"
/ strain="T89"
/ the taxon: 47664"
/ tissue type="leaf"
/ clone_lib="Populus strain T89 leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Liaboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .366
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-17 (1-30) x BI070561 (1-351)
Fax: 46 8 245452
Email: rikerl@biochem.kth.se.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rel: +55-11-2704922
                                                                                                                                                                                                                                                    117
57.00
66.67%
41.67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||::: |||
92 GGAGAATGATG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0737800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brazil
                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEPTINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
BI055877
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

à

à

```
CA931030 370 bp mRNA linear EST 30-DEC-2002 MTUZTA.PI.A09 Aspen apex CDNA Library Populus tremuloides CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Populus tremuloides (quaking aspen)
Populus tremuloides
Populus tremuloides
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Gamatophyta, eudicotyledons; core eudicots; rosids, euroside I, Manoliophyta, Salicaceae, Salicace, Populus.

| (bases 1 to 370)
| (bases 1 to 370)
| (Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="GN0330"
/note="Gryan: placenta normal; Vector: puc18; Site_l:
Smal; Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector: Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIleGlyGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublibates ......
Contact: Tead C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources (
Broironmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsaigmtu.edu.
Email: chtsaigmtu.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94490
008800
                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="texon:3693"
/clone lib="Aspen apex cDNA Library"
/note="Organ: apex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .370
/organism="Populus tremuloides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed sequence tags from Aspen Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-684-215B-17 (1-30) x CA931030 (1-370)
                                                                                                                                                                                                                                                                                                                                                                                                             (1-366)
                                                                                                                                                                                                                                                                                                                                                                                                             US-09-684-215B-17 (1-30) x BI055877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA931030
CA931030.1 GI:27419510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.00
66.67%
41.67%
38.51%
```

Mon May

g

ਨੇ

```
21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                        Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                 REFERENCE
AUTHORS
                                                                TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
CA932035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 bp mRNA linear EST 30-DEC-2002 MTU4TA.P25.F03 Aspen apex cDNA Library Populus tremuloides cDNA, CA931997
                                                                                                                                                                  CA931960 370 bp mRNA linear EST 30-DEC-2002 MIU4TA.P25.B07 Aspen apex cDNA Library Populus tremuloides cDNA,
                                                                                                                                                                                                                                                                 Populus tremuloides (quaking aspen)

Populus tremuloides

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Storida; eurosida il Malphghiales; Salicaceae; Saliceae; Populus.

(bases 1 to 370)

Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Populus tremuloides (quaking aspen)
Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle 20
                              146 ACATCTGGAGCAGAGGGATTCGAAGTGTTCCAAGGAGGATCAGGGTTCGCATTTCTCGCA 87
                                                                                                                                                                                                                                                                                                                                                                                                     Expressed sequence tags from Aspen Unpublished (2003) Contact: Tsai C-J Plant Biotech Research Center Michigan Technological University, School of Forest Resources &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370
10
6
8
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Populus tremuloides"
/mol type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen apex cDNA_Library"
/note="Organ: apex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-17 (1-30) x CA931960 (1-370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: chtsai@mtu.edu.
Location/Qualifiers
1. .370
                                                                                                                                                                                                                                  CA931960.1 GI:27420440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA931997.1 GI:27420477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.00
66.67%
41.67%
38.51%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||:::
285 GGAGAAATGATG 296
                                                              21 GlyGlnAlaMet 24
                                                                                                86 GGAGAAATGATG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyGlnAlaMet 24
                                                                                                                                                                                                    mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
DB:
                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
CA931997
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                  LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                  RESULT 10
CA931960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
```

g

ò

```
CA932035 370 bp mRNA linear EST 30-DEC-2002
MTU4TA.P26.All Aspen apex cDNA Library Populus tremuloides cDNA,
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Populus tremuloides (quaking aspen)
Populus tremuloides
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
1 (bases 1 to 370)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
Isai,C-J.
                                                                                                 Expressed sequence tags from Aspen
Unpublished (2003)
Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
Environmental Science
11400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expréssed sequence tags from Aspen
Umpublished (2003)
Contect: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 370)
Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
171: 906 487 2915
Fax: 906 487 2915
Email: chtsai@mtu.edu.
Loaninn/Qualifiers
L. 370
/organism="Populus tremuloides"
/mol_type="mRNA"
/db xref="texon:3693"
/clone_lib="Aspen apex cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370
10
8
0
0
                                                                                                                                                                                                                                                                                                                Email: chteai@mtu.edu.
Location/Qualifiers
1...570
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone lib="Aspen apex cDNA Library"
/note="Torgan: apex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215B-17 (1-30) x CA931997 (1-370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA932035
CA932035.1 GI:27420515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.00
66.67%
41.67%
38.51%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 GGAGAATGATG 296
```

```
CA932138.1 GI:27420618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 GCAGAAATGATG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity: Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
CA927770/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
        RESULT 14
CA932138
LOCUS
DEFINITION
                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                    CA932108 370 bp mRNA linear EST 30-DEC-2002 MTU4TA.P27.A02 Aspen apex cDNA Library Populus tremuloides cDNA, mRNA sequence.
CA932108.1 GI:27420588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Populus tremuloides (quaking aspen)
Populus tremuloides
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae, Populus.
1 (bases 1 to 370)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
                                                                                                                                                                                     1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle 20
                                                                                                                                                                      1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProlle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inter.V.U.

Expressed sequence tags from Aspen
Unpublished (2003)
Contact: Tsai C.J

Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2915
Fax: 906 487 2915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370
110
0
                                                370
10
6
8
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen apex cDNA Library"
/note="Organ: apex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-17 (1-30) x CA932108 (1-370)
                                                                                                                                            US-09-684-215B-17 (1-30) x CA932035 (1-370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: chtsai@mtu.edu.
Location/Qualifiers
/note="Organ: apex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126
57.00
66.67%
41.67%
38.51%
                                                   126
57.00
66.67%
41.67%
38.51%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 GGAGAATGATG 296
                                                                                                                                                                                                                                          |||::: |||
285 GGAGAAATGATG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GlyGlnAlaMet 24
                                                                                                                                                                                                                          21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsai, C-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                            RESULT 13
CA932108
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \dot{\delta}
                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                          8
                                                                                                                                                                        8
```

```
CA927770 374 bp mRNA linear EST 30-DEC-2002 MTUGTR.P12.G06 Aspen root cDNA Library Populus tremuloides CDNA, mRNA sequence.
CA927770 CA927770.1 GI:27416249
370 bp mRNA linear EST 30-DEC-2002
MTG/TA, P27.D05 Aspen apex cDNA Library Populus tremuloides cDNA,
CA932138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Populus tremuloides (quaking aspen)
Populus tremuloides
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Malpighiales, Salicaceae, Saliceae, Populus.
                                                                                                                                                                              Populus tremuloides (quaking aspen)
Populus tremuloides
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
I (bases I to 370)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlyGlyFleilalleProlle 20
                                                                                                                                                                                                                                                                                                                                                                         Expressed sequence tags from Aspen
Unpublished (2003)
Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources (
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2915
Fax: 906 487 2915
Email: chtsai@mtu.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (Dases 1 to 374) Ranjanales; Salicaceae; Saliceae; Popul Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Teai,C-J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370
66
60
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="texon:3693"
/olone lib="Aspen apex cDNA Library"
/note="Organ: apex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .370
/organism="Populus tremuloides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed sequence tags from Aspen Unpublished (2003) Contact: Tsai C-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-17 (1-30) x CA932138 (1-370)
```

```
57.00
66.67%
41.67%
38.51%
 41.67% 38.51%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||::: |||
86 GGAGAATGATG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GlyGlnAlaMet 24
                                                                                                                                     |||:::
86 GGGAAATGATG 75
                                                                                                                       21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
               Query Match:
DB:
                                                                                                                                                                     RESULT 17
CA928493/c
LOCUS
                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 18
CA928769/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed sequence tags from Aspen
Unpublished (2003)
Contact: Tsai C-J
Contact: Tsai C-J
Contact: Tsai C-J
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.
LocationfQualifiers
rce
                                                                                                                                                                                                                                                                                                                                                                                                                       374 bp mRNA linear EST 30-DEC-2002
MTGTR.P2.G12 Aspen root cDNA Library Populus tremuloides cDNA,
CA928449
Populus tremuloides (quaking aspen)
Populus tremuloides
Populus tremuloides
Eukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
I (bases I to 374)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
                                                                                                                                                                                                                                                                                                                                  1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="texxon:3693"
/clone lib="Aspen root cDNA Library"
/note="Organ: root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374
10
6
                                                                                                                                                                                                          374
10
6
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                             US-09-684-215B-17 (1-30) x CA927770 (1-374)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA928449.1 GI:27416928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127
57.00
66.67%
                                                                                                                                                                                                          127
57.00
66.678
41.678
38.518
                                                                                                                                                                                                                                                                                                                                                                     21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                   |||:::
86 GGAGAAATGATG 75
                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 16
CA928449/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                       FEATURES
                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                      ò
```

```
Dest Ymatch: 14.574 Mismatches: 8

Ousery Match: 14.574 Mismatches: 8

Dest Ymatch: 14.574 Mismatches: 8

Ousery Match: 15.514 Gaps: 0

Ousery Match: 15.517 (1-30) x CA928449 (1-374)

Out 11.512.71 (1-30) x CA928449 (1-374)

Out 11.522.71 (1-30) x CA928449 (1-374)

Out 11.522.71 (1-30) x CA92849 (1-374)

Out 11.522.71 (1-30) x CA92849 (1-374)

Out 12.522.71 (1-30) x CA92849 (1-374)

Out 13.522.71 (1-30) x CA92849 (1-374)

Out 13.522.72 (1-374)

Ou
```

```
CA931394 385 bp mRNA linear EST 30-DEC-2002
MTUZTA.P6.G03 Aspen apex CDNA Library Populus tremuloides CDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Malpighiales, Salicaceae, Saliceae, Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                    1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2003)
Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.
1. 385
                                                                                                                                                                                                                                                                                                                                                             146 ACATCTGGAGCAGAGGGATTCGAAGTGTTCCAAGGAGGATCAGGGTTCGCATTTCTCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 385)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai,C-J.
Expressed sequence tags from Aspen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="texcon:3693"
/clone lib="Aspen apex cDNA Library"
/note="Organ: apex"
                                                                                                                                                                          384
0 0 8 0 0 0
                                                 /mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen apex cDNA_Library"
/note="Organ: apex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Populus tremuloides"
                  1. .384
/organism="Populus tremuloides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Populus tremuloides (quaking aspen)
Populus tremuloides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-17 (1-30) x CA931394 (1-385)
                                                                                                                                                                                                                                                                                                    US-09-684-215B-17 (1-30) x CA931116 (1-384)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA931394.1 GI:27419874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132
57.00
66.67%
41.67%
38.51%
                                                                                                                                                                                           57.00
66.67%
41.67%
38.51%
                                                                                                                                                                                                                                                                                                                                                                                                                                             86 GCAGAAATGATG 75
                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
CA931394
                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA931394/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                      source
                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                              ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA931116

MTUZTA.P2.D03 Aspen apex cDNA Library Populus tremuloides cDNA, mRNA sequence.

CA931116.1 GI:27419596
                                Populus framiloides superiors, iquaning aspen)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus. I (bases I to 374)
Tsaia, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Populus tremuloides (quaking aspen)
Populus tremuloides
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Malpighiales, Salicaceae, Saliceae, Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProlle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Teal C-J'
Contact: Teal C-J'
Plant Biotech Research Center
Michigan Biotech Research Conter
Michigan Science
Buvironmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
                                                                                                                                                                            Expréssed sequence tags from Aspen
Unpublished (2003)
Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 384)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374
10
6
0
0
                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:3693"
/clone lib="Aspen root cDNA Library"
/note="Organ: root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                             organism="Populus tremuloides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed sequence tags from Aspen Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-684-215B-17 (1-30) x CA928769 (1-374)
                                                                                                                                                                                                                                                                                                    Tel: 906 487 2914

Fax: 906 487 2915

Email: chtsai@mtu.edu.

Location/Qualifiers

1. 374
   GI:27417250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: chtsai@mtu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127
57.00
66.67%
41.67%
38.51%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||::: |||
86 GGAGAAATGATG 75
   CA928769.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ßai, C−J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 19
CA931116/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                       ORGANISM
                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                           REFERENCE
AUTHORS
 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
```

d ò

8

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

CA931501/c LOCUS

RESULT 21

g

ð

임

```
388 bp mRNA linear EST 30-DEC-2002
MTUGTR.P11.C07 Aspen root cDNA Library Populus tremuloides cDNA,
CA927636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Sosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
1 (bases 1 to 388)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed sequence tags from Aspen
Unpublished (2003)
Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2914
Email: chtsaiemtu.edu.
Location/Qualifiers
1. 387
/mol type="mRNA"
/mol type="mRNA"
/db_xref="taxon:3693"
/clone lib="Aspen apex cDNA Library"
/note="Organ: apex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ThralaalaaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Task 2-0.

Contact: Task 2-0.

Plant Biotech Research Center

Michigan Technological University, School of Forest Resources & Environmental Science.

1400 Townsend Drive, Houghton, MI 49931-1295, USA

Tel: 906 487 2914

Fax: 906 487 2915

Email: chtaidmtu.edu.

Location/Qualifiers

1. 388

/organism="Populus tremuloides"
      1 (bases 1 to 387)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P.
Tsai,C-J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387
10
6
6
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mgNA"
/db_xref="taxon:3693"
/clone_lib="Agpen root cDNA Library"
/note="Organ: root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Populus tremuloides (quaking aspen)
Populus tremuloides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed sequence tags from Aspen
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-684-215B-17 (1-30) x CA931767 (1-387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA927636.1 GI:27416115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133
57.00
66.67%
41.67%
38.51%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 GGAGAAATGATG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                               TITLE
JOURNAL
COMMENT
        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 23
CA927636
                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                    CA931501

385 bp mRNA linear BST 30-DEC-2002 MTUJTA.P8.B06 Aspen apex CDNA Library Populus tremuloides CDNA, mRNA sequence.
CA931501. GI:27419981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA931767 387 bp mRNA linear EST 30-DEC-2002 MTU4TA.P22.F11 Aspen apex cDNA Library Populus tremuloides cDNA,
                                                                                                                                                                                                                                                                                                       Populus tremuloides (quaking aspen)
Populus tremuloides
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dopulus tramuloides (quaking aspen)
Populus tramuloides
Populus tramuloides
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
146 ACATCTGGAGCAGGGATTCGAAGTGTTCCAAGGAGGATCAGGGTTCGCATTTCTCGCA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expréssed sequence tags from Aspen
Unpublished (2003)
Contact: Tsal C-J
Flant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 385) Ranjan, P., Xao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38
0 9 8 9 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Populus tremuloides"
/mol_type="mRNA"
/db_txef="taxon:3693"
/dlone lib="Aspen apex cDNA Library"
/note="Organ: apex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-17 (1-30) x CA931501 (1-385)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: chtsai@mtu.edu.
Location/Qualifiers
1. .385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
CA931767
CA931767.1 GI:27420247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.67%
41.67%
38.51%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.00
                                                                 GlyGlnAlaMet 24
                                                                                         |||::: |||
86 GGAGAAATGATG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||:::
GGAGAAATGATG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                 21
```

Query Match: DB:

d ઠે

ઠે

. No.:

Score:

ORIGIN

VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

ACCESSION

RESULT 22 CA931767 LOCUS

```
CA927727 Thear EST 30-DEC-2002 MTWTR. Pl2.C07 Aspen root cDNA Library Populus tremuloides cDNA, CA927727 CA927727
                  ARJOURE BY THE ASPEN TOOL CDNA Library Populus tremuloides CDNA, MANA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Populus tremuloides (quaking aspen)
Populus tremuloides
Populus tremuloides
Populus tremuloides
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
I (bases I to 389)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
Tsai,C.J.
Expressed sequence tags from Aspen
Umpublished (2003)
Umpublished (2013)
Plant Biotech Research Center
                                                                                                                                    Populus tremuloides (quaking aspen)
Populus tremuloides
Populus tremuloides
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
I (bases I to 388)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
                                                                                                                                                                                                                                                                        Expressed sequence tags from Aspen Unpublished (2003) (Contact: Tsai C-J Plant Biotech Research Center Michigan Technological University, School of Forest Resources & Environmental Science 11400 Townsend Drive, Houghton, MI 49931-1295, USA Tel: 906 487 2915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Populus tremuloides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:3693"
/clone lib="Aspen root
/note="Organ: root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-684-215B-17 (1-30) x CA929028 (1-388)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: chtsai@mtu.edu.
Location/Qualifiers
1. .388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA927727.1 GI:27416206
                                                                                                       CA929028.1 GI:27417509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.00
66.67%
41.67%
38.51%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||:::
86 GGAGAAATGATG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity: 6
Best Local Similarity: 4
Query Match: 5
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 26
CA927727/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
RESULT 25
CA929028/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ed No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                             CA928025 388 bp mRNA linear EST 30-DEC-2002 MTU6TR.P15.H06 Aspen root cDNA Library Populus tremuloides cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids, eurosids I; Malpighiales, Salicaceae, Saliceae, Populus.
                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProlle 20
                                                                                                                                                                                                                 1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPhealaileProile 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 ACATCTGGAGCGAGCGATTCGAAGTGTTCCAAGGAGGATCAGGGTTCGCATTTCTCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Injuriantal (2015)
Contact: Tasi C-7
Contact: Tasi C-7
Plant Biotech Research Center
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources (
Britishmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.
Location/Qualifiers
1.388
1.388
/organism="Populus tremuloides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 388)
Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     988
098
008
008
                                                    388
110
6
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /moi_type="mRNA"
/db_xref="texon:3693"
/clone_lib="Aspen root cDNA Library"
/note="Organ: root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Populus tremuloides (quaking aspen)
Populus tremuloides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed sequence tags from Aspen Unpublished (2003)
                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-17 (1-30) x CA928025 (1-388)
                                                                                                                                                                               US-09-684-215B-17 (1-30) x CA927636 (1-388)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA928025
CA928025.1 GI:27416504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134
57.00
66.67%
41.67%
38.51%
                                                    134
57.00
66.67%
41.67%
38.51%
                                                                                                                                                                                                                                                                                                           |||:::
303 GGAGAAATGATG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||::: |||
86 GGAGAAATGATG 75
                                                                                                                                                                                                                                                                                     21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sai, c-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sig
Query Match:
DB:
                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                           RESULT 24
CA928025/c
                                                        . No. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                     ö
```

```
CA927617.1 GI:27416096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
CA927744
CA927744.1 GI:27416223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.00
66.67%
41.67%
38.51%
     38.51%
14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 GGAGAAATGATG 316
                                                                                                                                              |||:::
86 GGAGAAATGATG 75
                                                                                                                              21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                        CA92761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
     Query Match:
DB:
                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA927744/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
COMMENT
                                                                                                                                                                                    RESULT 28
CA927617
                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               සු
                                                                       8
                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA928142 30-DEC-2002 MRNA linear EST 30-DEC-2002 MTU6TR.P17.C03 Aspen root cDNA Library Populus tremuloides cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosida I, Malpighiales; Salicaceae; Saliceae; Populus. (bases 1 to 389)
                                                                                                                                                                                                                                                                                                                                                   1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                  Tsai, C-J.

Expressed sequence tags from Aspen
Unpublished (2003)
Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Bryironmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Michigan Technological University, School of Forest Resources Environmental Science
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2915
Fax: 906 487 2915
Email: chesidentu-edu.
Location/Qualifiers
                                                                                             1. .389
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen root cDNA Library"
/note="Organ: root"
                                                                                                                                                                                                                          389
6 0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="texon:3693"
/clone lib="Aspen root cDNA Library"
/note="Grgan: root"
                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Populus tremuloides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Populus tremuloides (quaking aspen)
Populus tremuloides
                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                        US-09-684-215B-17 (1-30) x CA927727 (1-389)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: chtsai@mtu.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA928142.1 GI:27416621
                                                                                                                                                                                                                       134
57.00
66.67%
41.67%
38.51%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
57.00
66.67%
41.67%
                                                                                                                                                                                                                                                                                                                                                                                                                          |||:::
86 GGAGAAATGATG 75
                                                                                                                                                                                                                                                                                                                                                                                                          GlyGlnAlaMet 24
                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                              Query Match:
DB:
                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 27
CA928142/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
390 bp mRNA linear EST 30-DEC-2002 MTUGTR:P11.A10 Aspen root cDNA Library Populus tremuloides cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA927744 390 bp mRNA linear EST 30-DEC-2002 MTUGTR.P12.E03 Aspen root cDNA Library Populus tremuloides cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Malpighiales, Salicaceae, Saliceae, Populus.
1 (Dases 1 to 390)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 ACATCTGGAGCAGGAGGGATTCGAAGTGTTCCAAGGAGGATCAGGGTTCGCATTTCTCGCA 304
                                                                                                                       1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle 20
                                                                                                                                                              146 ACATCTGGAGGAGGATTCGAAGTGTTCCAAGGAGGATCGGGGTTCGCATTTCTCGCA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expréssed sequence tags from Aspen
Unpublished (2003)
Contact: Tsai C.J.
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00 8 6 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: chtsai@mtu.edu.
Location/Qualifiers
1.390
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_tref="taxon:3693"
/clone lib="Aspen root cDNA Library"
/note="Grgan: root"
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Populus tremuloides (quaking aspen)
Populus tremuloides
Indels:
Gaps:
                                                                  US-09-684-215B-17 (1-30) x CA928142 (1-389)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215B-17 (1-30) x CA927617 (1-390)
```

```
Alignment Scores:
                                                                                                                                                                                                                         Query Match:
DB:
                                                                                                                                                            Pred. No.:
                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA927930 390 bp mRNA linear EST 30-DEC-2002
MTUGTR.P14.F11 Aspen root cDNA Library Populus tremuloides cDNA,
             Populus tremuloides (quaking aspen)

Populus tremuloides

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Trachas, eurosida; I, Malpighiales; Salicaceae; Saliceae; Populus.

(Dases 1 to 390)

Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
(bases 1 to 390)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlalleProlle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 ACATCTGGAGCGAGGGATTCGAAGTGTTCCAAGGAGGATCAGGGTTCGCCA 87
                                                                                                                                                                       Unpublished (2003)
Contact: Tsai C-J
Plant Blotceh Research Center
Michigan Technological University, School of Forest Resources & Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsaiemtu.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /moi_type="mRNA"-
/db_xref="texaon:3693"
/dlone_lib="Aspen root cDNA Library"
/note="Organ: root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. 390
/organism="Populus tremuloides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Populus tremuloides (quaking aspen)
Populus tremuloides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed sequence tags from Aspen
Unpublished (2003)
                                                                                                                                                          Expressed sequence tags from Aspen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-215B-17 (1-30) x CA927744 (1-390)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA927930.1 GI:27416409
                                                                                                                                                                                                                                                                                                                          chtsai@mtu.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134
57.00
66.67%
41.67%
38.51%
                                                                                                                                                                                                                                                                                  Tel: 906 487 2914
Fax: 906 487 2915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyGlnAlaMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 ĠĠAGAAATGÁŢĠ 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
CA927930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rsai, C-J
                                                                                                                                            rsai, C-J
                                                                                                                                                                                                                                                                                                                      Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 30
CA927930/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.:
               SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                        TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                    REFERENCE
AUTHORS
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           염
```

Run on:

Title:

```
Aas64141 Human /M.
Aca59949 Prostate
Ab15512 Ran2- P77
Acc95676 Prostate
Adb14284 Human pro
Abk39768 DNA encod
Aca12097 Human lun
Aca03283 Lung canc
Aca47078 Mycobacte
                                                  M. tuberc
M. tuberc
M. tuberc
                                                                                                                              Mycobacte
Mycobacte
Nucleotid
                                                                                                                                                                                                                                                                                                                                              Human pro
Mycobacte
Nucleotid
DNA encod
Human lun
Lung canc
DNA encod
Human Ral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lung canc
Human col
Ra12/C-te
Human lun
Lung tumo
Ra12-P775
                                                                                                                                                                                                                                         Human /M.
Prostate
Ra12- P51
Prostate
                                                                                                                                                                                                                Ra12-P510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lung tumour; cancer; T cell; immune response stimulator; cytostatic;
Aav44342 MAav444342 MAav644450 MAax19252 MAad803708 MAd28339 MAd2839 MAd2849 MAD8192 MAD8192 MAD8192 MAD8192 MAD8192 MAD8291 MAD82910 MAD82910 MAD82910 MAD82910 MAD82910 MAD82910 MAD8291 MAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                  AAZ19046
AAZ19252
AAX219252
AAX1928339
AAL40772
AAL40772
AAL40772
AAZ20206
AAZ20206
AAZ20206
AAZ20206
AAZ20206
AAZ20206
AAZ20206
AAZ20206
AAZ00208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACC95676
ADB14284
ABK39768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACA12097
ACA03283
AAD47078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding Ral2S-L985PEx peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUL-2000; 2000US-00614124.
29-AUG-2000; 2000US-00651563.
08-SEP-2000; 2000US-00658824.
26-SEP-2000; 2000US-00671325.
06-OCT-2000; 2000US-00702005.
13-DEC-2000; 2000US-0070205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK39777 standard; cDNA; 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-2001; 2001WO-US022058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORIXA CORP
  WO200204514-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene; sa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK39777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK39777
ID ABK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
     ONORELETAMENT PARAMENT | DEVENTH | D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encod
Human His
Lung canc
Nucleotid
Human DNA
RA12 (8) -
Mycobacte
Mycobacte
                                                                                                                                                                                 April 29, 2004, 20:30:12; Search time 85.3349 Seconds (without alignments) 1493.479 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abk39777 II
Aca12106 H
Aca03292 II
Aa140769 N
Ab671801 H
Aat91403 N
Aat91466 N
                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                    nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                        148
1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQI 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3373863 segs, 2124099041 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                          7.00.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK39777
ACA12106
ACA03292
AAL40769
ABS71801
AAD60769
AAT91403
                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62

Qaapop 10.0 , Xgapext

Ygapop 10.0 , Ygapext

Fgapop 6.0 , Fgapext

Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genesequ2001bs:*
genesequ2002s:*
genesequ2003as:*
genesequ2003cs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genesegn1980s:*
genesegn1990s:*
genesegn2000s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      geneseqn2001as:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           geneseqn2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N Geneseq 29Jan04:*
1: geneseqn1980s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                               US-09-684-215B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1000.0
1000.0
1000.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                    OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
```

2 2 4 5 9 6 7 8

Result No.

Switzer AP, Mcneill PD;

Wang T,

Wang A,

Fanger GR,

Bangur CS,

WANG T. SWITZER A H MCNEILL P I

(WANG/) (SWIT/) (MCNE/) (CLAP/)

```
The invention describes an isolated polymucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polymucleotide and/or polympeptide is useful for treating a lung cancer in a patient. The polymucleotide is useful for removing tumour calls from a biological sample. The polymucleotide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This sequence encodes a lung tumour associated protein or protein described in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but two. was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 ACGGCCCCCGATAACTICCAGCTGTCCCAGGGTGGCAGGGATTCGCCATTCGCCATC 81
                                       Mcnabb A;
                                                                                                                                            Novel polynucleotide encoding a lung tumor polypeptide useful for stimulating and/or expanding T cells specific for a tumor protein
             Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS,
Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 186 BP; 39 A; 61 C; 47 G; 39 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186
000
000
000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                    Claim 1; SEQ ID NO 1879; 223pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-684-215B-17 (1-30) x ABK39777 (1-186)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.916-15
148.00
100.00%
100.00%
                                                                                         WPI; 2002-164634/21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                           P-PSDB; AAU85595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACA12106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \stackrel{>}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

```
Human; lung cancer; ss; lung tumour; cytostatic; vaccine; T cell expansion; CD4; CD8; RA12; gene.
                                          Human His-tagged Ral2S-L985PEx fusion protein cDNA.
 ВP.
ACA12106 standard; cDNA; 186
                            (first entry)
                                                                                                   US2002197669-A1
                                                                             Homo sapiens
                            06-JUN-2003
                                                                                      Synthetic.
              ACA12106;
```

ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGheAlaIleProIle

8

03-MAY-2001; 2001US-00849626.

26-DEC-2002.

13-DEC-2000; 2000US-00736457

(BANG/) BANGUR C S. (FANG/) FANGER G R. (WANG/) WANG A.

```
The invention relates to a polymuclectide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in the specification, or a sequence (S2) mentioned in specification.

CC (maplement of S1, sequences consisting of at least 20 contiguous residues (CC of S1, sequences having 75%, preferably (CC of S1, sequences than hybridise to S1, Also included are an isolated polympeptide (comprising a sequence (S3) selected from any one of the 4 amino acid sequences mentioned in the specification, a sequence conded by the polymuclectide, or sequence encoded by the polymuclectide, or expension overtor comprising the polymuclectide, an expression overtor comprising the polymuclectide, and the vector, an isolated anibody (or its antigen binding fragment) that specifically binds to the polympeptide, detecting the present of a cancer in a patient, a fusion protein comprising the polympeptide, an olithonis, stimulating and/or expanding T cells specific for a tumour protein (comprising contacting) relis with the polymuclectide, protein conditions, stimulation and/or expanding T cells specific for a tumour protein (comprising contacting) relis with the polymuclectide, protein or antigen presenting cells, under conditions and for a time sufficient to permit the stimulation and/or expanding T cells and inhibiting the development of a cancer in presenting cells that express the polymuclectide, protein or projection or antigen proper sequence in a patient with the polymuclectide, protein or projection for stimulating an immune response in a patient, and for the protein or projection or the polymuclectide, protein and sequence of a cancer in a patient. The polymuclectide, protein compositions, e.g. vaccines. The polymuclectide is also useful as a protein compositions, e.g. vaccines. The polymuclectide is a patient (particular product of a cond hybridisation, and in
                                                                                                                                                                                                                      Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 186 BP; 39 A; 61 C; 47 G; 39 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-684-215B-17 (1-30) x ACA12106 (1-186)
                                                                                                                                                                                                                                                                                                           Example 10; Page; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.91e-15
148.00
100.00%
100.00%
100.00%
                                                                                                                                                             WPI; 2003-352750/33.
P-PSDB; ABU69570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                     Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
```

m

Page

20

22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGATGGGGCAGGGATTCGCCATTCCGATC 81

30

82 gegenegegenegegenegegegenen 111

21 GlyGlnAlaMetAlaIleAlaGlyGlnIle

ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle

US-09-684-215B-17 (1-30) x ACA03292 (1-186)

us-09-684-215b-17.rng

```
The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polynucleotide associated with the compositions and methods for the therapy and diagnosis of lung cancer
22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide, useful for preparing a composition for treating inhibiting development of cancer, e.g. lung cancer.
                                                                                                                                                                                                                                       Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watanabe Y, Johnson JC, Retter MW;
inger GR, Vedvick TS, Bangur CS, M
                                                                                                                                                                                                          Lung cancer therapyand diagnosis associated cDNA #1767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 186 BP; 39 A; 61 C; 47 G; 39 T; 0 U; 0 Other;
                                              GGCCAGGCGATGGCGATCGCGGGCCAGATC 111
                            GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; SEQID NO 1879; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Henderson RA, Wang T, Watanabe
Durham M, Carter D, Fanger GR,
                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-1999, 99US-00346492.
15-OCT-1999; 99US-00419356.
17-DEC-1999; 99US-00466667.
30-DEC-1999; 99US-00476607.
22-MAR-2000; 2000US-00519642.
22-MAR-2000; 2000US-00519642.
27-APR-2000; 2000US-00546259.
27-APR-2000; 2000US-00546259.
11-JUL-2000; 2000US-0061124.
29-AUG-2000; 2000US-0065153.
26-SEP-2000; 2000US-00671325.
66-CCT-2000; 2000US-00671325.
13-DEC-2000; 2000US-00671419.
30-OCT-2000; 2000US-0077419.
                                                                                                                    ACA03292 standard; cDNA; 186
                                                                                                                                                                                                                                                                                                                                                             10-JUL-2001; 2001US-00902941
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-328427/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                    US2002172952-A1.
                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                             22-MAY-2003
                                                                                                                                                                                                                                                                                                                                21-NOV-2002.
                            21
                                                                                                                                                 ACA03292;
                                                                                                    RESULT
                            ð
```

```
The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 kba in an an infrastance of the comprising a polynucleotide sequence of the compinant fragment of serine protease antigen MTB32A of the recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                          Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis;
vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
immunogen; cytokine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 396 BP; 68 A; 132 C; 134 G; 62 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                            'note= "No start or stop codon"
                                                                                                                                           Nucleotide sequence encoding Ra12 protein.
                                                                                                                                                                                                                                                                                                                                         "Ral2 protein"
                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .396
/*tag= a
/product= "Ral2 prote
                                  琚.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1, Fig 2, 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-OCT-2000; 2000WO-US027652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0158585P.
                                  AAL40769 standard; DNA; 396
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky Y, Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-266299/27.
P-PSDB; AA022138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                               WO200125401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-OCT-1999;
                                                                                                         03-OCT-2002
                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2001.
                                                                      AAL40769;
                 AAL40769
RESULT
```

ŏ

Alignment Scores:

186 000 000

Length:
Matches:
Conservative:
Mismatches:
Indels:

2.91e-15 148.00 100.00% 100.00%

Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores: Pred. No.:

```
AAD60769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FOYT/) 1
(HOUG/) 1
(REED/) 1
                                                                                                                                                                                                                                                                                                                                                                                                8888888888888888
                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polypeptide (I) comprising 7-30 consecutive amino acid residues of human mammaglobin, where one or more mammaglobin specific T cells specifically reacts with (I). Also included the armaglobin specific T cells specifically reacts with a physiologically acceptable carrier or immunostimulant; (2) a diagnostic kit, comprising (I), in compination with a physiologically acceptable carrier or immunostimulant; (2) a diagnostic kit, comprising the forestion reagent comprising a reporter group; (3) removing tumour cells from a biological sample, by contacting a biological sample with T cells that specifically react with (I), under conditions and for a time sufficient to permit the removal of cells conditions and for a time sufficient to permit the sample; (4) and isolated T cell population (II), comprising T cells prepared using (I), and (5) a composition (II), comprising a poly.uclectide comprising a not affinity tag), or a polypeptide comprising a human mammaglobin (or variant or tagged with an affinity tag), in combination with an
                                                                                                                                  1 Acedocadoriccarinocadoriccadoricadoridada anticocarinocarino en
                                                                                                           ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptides comprise one or more human mammoglobin epitopes and polynucleotides encoding the polypeptides, useful for preventing and treating breast cancers.
                                                                                                                                                                                                                                                                                                                                Human, epitope, mammaglobin, breast cancer, cytostatic, T cell; CD4+; CD8+; antigen; RA12; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang A, Johnson JC, Mcneill PD,
                                                                                                                                                                                                                                                                                                              Human DNA encoding a mammaglobin/RA12 fusion protein.
      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                       GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                         GGCAGGCGATGCCGAGGCCAGATC 90
                                                                Gaps:
                                                                                     (1-396)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 115; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TM, Clapper JD,
                                                                                  US-09-684-215B-17 (1-30) x AAL40769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JAN-2001; 2001US-00757417.
7.45e-15
148.00
100.00$
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JAN-2002; 2002WO-US003057
                                                                                                                                                                                                                              ABS71801 standard; DNA; 399
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-706844/76.
P-PSDB; ABG94684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fling SP, Foy
Sutherland RA;
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200253017-A2.
                                                                                                                                                                                                                                                                           29-AUG-2003
02-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                Chimeric.
                                                                                                                                                                                                                                                      ABS71801;
                                                                                                                                                          21
                                                   Query Match
DB:
     No.:
                                                                                                                                                                                                                 RESULT
                                                                                                                                                         ò
```

```
immunostimulant. The peptide is useful for inhibiting the development of breast cancer in a patient, by incubating CD4+ and/or CD8+ T cells isolated from a patient with a mammoglobin epitope, such that T cells proliferate, administering the proliferated T cells to the patient, optionally cloning at least one proliferated T cell and administering at least one cloned cell, and thus inhibiting the development of breast cancer in the patient. The compositions and methods are useful for sequence encodes a human mammaglobin/RA12 fusion protein. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic, epitope, mammaglobin, mgb, therapy, breast cancer, diagnosis, vaccine, human, chimeric, fusion protein, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ACGGCGCGCCCGATAACTICCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide epitopes of human mammaglobin useful in inhibiting development of breast cancer and in breast cancer diagnosis and monitoring, and to produce antibodies also useful in breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a //tag= a //tag= //tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 399 BP; 109 A; 96 C; 92 G; 102 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ra12 (s) -human MammFL chimeric DNA construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghton RL, Reed SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-215B-17 (1-30) x ABS71801 (1-399)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JAN-2001; 2001US-00757417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000; 2000US-00580376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.52e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD60769 standard; DNA; 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric- Homo sapiens.
Chimeric- Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOY I M. HOUGHION R L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-776615/73.
P-PSDB; ABW00067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fanger GR, Foy TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FANG/) FANGER G R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REED S G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2002082216-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUN-2002.
```

WPI; 1997-192904/17. P-PSDB; AAW32354.

us-09-684-215b-17.rng

```
The present invention provides polypeptide epitopes of human mammaglobin (mgb) useful for the therapy, diagnosis and monitoring of breast cancer. The invention is related to specific epitopes of mammaglobin, to antibodies and immune cells that recognise such epitopes and to methods for detecting mammaglobin in patient serum. These peptides, antibodies and cells may be useful in vaccines and pharmaceutical compositions for prevention and treatment of breast cancer. The invention is also useful to detect and /or monitor the progression of breast cancer. The present sequence is Ral2 (s)-human MammFL chimeric DNA construct used in the expression of recombinant Ral2(s) MammFL, a fusion protein consisting of full length human mammaglobin with short Ral2. This protein is used in the exemplification of the invention
diagnosis and monitoring
                                                    Example 8; Page 29; 66pp; English
```

Sequence 399 BP; 109 A; 96 C; 92 G; 102 T; 0 U; 0 Other;

```
20
                                                                                                                                     8
                                                                                                                              22 ACGGCCCCCGTCCCGATAACTTCCCACTGTCCCAGGGTGGGCAGGAATTCGCCATTCCCATC
                                                                                                                ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                    82 gegekagecgangecgancecggeccagane 111
                                                                                                                                                            GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                   Gaps:
                                                                                         (1-399)
                                                                                          US-09-684-215B-17 (1-30) x AAD60769
           7.52e-15
148.00
100.00%
100.00%
                                  Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                                                                                                                                             21
                                                         Query Match:
DB:
                                                                                                                 8
                                                                                                                                                            ð
                                                                                                                                                                                 g
```

Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis; ss. Mycobacterium tuberculosis antigen TbRa12 encoding DNA. ВР AAT91403 standard; DNA; 447 Mycobacterium tuberculosis 12-JAN-1998 (first entry) AAT91403 AAT9140 RESULT

/product= "Antigen_TbRal2" Location/Qualifiers 11. .409 /*tag= a 95US-00523435. 95US-00532136. 96US-00620280. 96US-00658800. 96WO-US014675 96US-00680573 (CORI-) CORIXA CORP 22-SEP-1995; 22-MAR-1996; 05-JUN-1996; 12-JUL-1996; WO9709429-A2 30-AUG-1996; 01-SEP-1995; 13-MAR-1997

CORP

(CORI-) CORIXA

Houghton

Campos-Neto A,

Skeiky YAW, Dillon DC, I, Twardzik DR;

Reed SG, Sk Vedvick TH,

```
A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence encodes a specifically claimed M. tuberculosis antigen, Tbhall. The immunogenic polypeptide can be used to diagnose M. tuberculosis in frection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic princers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 acceccecercearaacriccaecrerccaecresescaesescaraescarreceare 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
                                                     New immunogenic polypeptide(s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis; ss.
                                                                                                                                                                                                                                                                                      Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis antigen TbRa12 encoding DNA
                                                                                                                                                                                                                                                                                                                                 44 0
0 0
0 0
0 0
                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eccedecearecearececececeare 100
                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "Antigen_TbRa12"
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-17 (1-30) x AAT91403 (1-447)
                                                                                                Claim 3; Page 49-50; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             멾
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-00523436.
95US-00533634.
96US-00620874.
96US-00659683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US014674.
                                                                                                                                                                                                                                                                                                                              8.66e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT91466 standard; DNA; 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .409
                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9709428-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JAN-1998
                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-1995;
22-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT91466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                    ..
00
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT91466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
```

```
A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence encodes a specifically claimed M. tuberculosis antigen, TbRal2. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ACGGCCGCCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 70
                                                                                  New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
            Houghton R;
                                                                                                                                                                                                                                                                                           Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Puberculosis; infection; diagnosis; antigen; TbRa12; ss.
                                                                                                                                                                                                                                                                                                                                 44 0
0 0
0 0
0 0
            Campos-Neto A,
                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis antigen TbRal2 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCAGGCGATGCCCGGCCCAGATC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis; strain H37Ra.
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-684-215B-17 (1-30) x AAT91466 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                    Claim 3; Page 50; 168pp; English.
          Dillon DC,
DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-00729622.
97US-00818111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US018214
                                                                                                                                                                                                                                                                                                                              8.66e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV44342 standard; DNA; 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11. .406
/*tag= a
          Skeiky YA,
I, Twardzik
                                               WPI; 1997-192903/17.
P-PSDB; AAW32422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-1996;
13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2003
09-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9816645-A2
          Reed SG, Sk
Vedvick TH,
                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV44342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

```
Thrais Case AAWG4294). It was isolated from a M. tuberculosis strain things appearant to the invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAWG4291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also calained are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ů
                                                                                                                                                                    This DNA sequence codes for Mycobacterium tuberculosis soluble antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculosis, immunogenic, soluble, antigen, protective immunity, TB, vaccine, pharmaceutical, infection, diagnosis, ss.
                                                                             New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houghton R;
Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
5, Twardzik DR, Lodes MJ;
                                                                                                                                                                                                                                                                                                                                                                        BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M. tuberculosis immunogenic polypeptide TbRa12 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degcadeceardecearcecedecearc 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-17 (1-30) x AAV44342 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ď,
                                                                                                                                          Claim 3; Page 61; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US018293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-00730510.
97US-00818112.
                                                                                                                                                                                                                                                                                                                                                                                                               8.66e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV64450 standard; DNA; 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                          WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                        P-PSDB; AAW64294
                                                                                                                                                                                                                                                                                                                                                                         Sequence 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9816646-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-1996;
13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-1999
Reed SG, Sk
Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV64450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                    No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV64450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \dot{\delta}
```

```
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9942076-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                           05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reed SG, Sk
Vedvick TS,
                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-1999
                                                                                                                                                                                                                                                                                                                         AAZ19252;
                                                                                                                                                       Query Match:
DB:
                                                                                                                  ..
Ю
                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                            AAZ19252
                                                                                                                                                                                                                                                                                                      ¥88888888¥&
                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                       11 ACGGCCCCCCATAACTTCCCAGCTGTCCCAGGGTGGCCAGGATTCCCCATTCCCATC 70
                                           Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis.
                                                                                                      This sequence encodes an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                            ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen; diagnosis, detection; infection; antibody; immunisation; vaccine; immunity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide comprising antigenic portions of M. tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ᇝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biky YAW, Dillon DC, Campos-Neto A, Houghton Twardzik DR, Lodes MJ, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. tuberculosis recombinant antigen DNA encoding TbRa12.
                                                                                                                                                                         Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;
                                                                                                                                                                                                       447
00
00
00
00
                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                   GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                         US-09-684-215B-17 (1-30) x AAV64450 (1-447)
                                                                                      Claim 3; Page 62-63; 230pp; English,
 Lodes MJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 103; 323pp; English
                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00024753
98US-00072596
                                                                                                                                                                                                       8.66e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                             AAZ19040 standard; DNA; 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
 Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky YAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-527416/44.
P-PSDB; AAY38959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                  WPI; 1998-261042/23
                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                              P-PSDB; AAW81657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed SG, Sk
Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9942118-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAY-1998;
                                                                                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1999
 Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ19040;
                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                        셤
 ò
                                                                                                                                                                                                                                                                                                                                    ò
```

```
The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 ACGCCCCCCTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCATTCCGATTC 70
This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houghton R; RC;
                                                                                                                                                                                                                                      Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                             444
30
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campos-Neto A,
I, Hendrickson
                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M. tuberculosis antigen TbRa12 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCAGGCGATGCCGGGGCCAGATC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyGlnAlaMetAlaileAlaGlyGlnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-684-215B-17 (1-30) x AAZ19040 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky YAW, Dillon DC, Car
, Twardzik DR, Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 73; 299pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           멾
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US003268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00025197.
98US-00072967.
                                                                                                                                                                                                                                                                                                                    8.668-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ19252 standard; DNA; 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-527409/44.
P-PSDB; AAY39096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
```

```
humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antiques that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, AIDS
                                                                                                                                                                  US-09-684-215B-17 (1-30) x AAS03780 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 83; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guderian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-2002; 2002WO-US008223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-2001; 2001US-0275837P
                                                                                         66e-15
                                                                                                                                                                                                                                                                                                  AAD47080 standard; DNA; 447
                                                                                                148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky Y, Brannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-759844/82.
P-PSDB; AAE29705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP
                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200272792-A2
                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                             27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-2002
                                                                                                                                                                                                                                                                                                                         AAD47080;
                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                     AAD47080
                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence encodes Mycobacterium tuberculosis TbRa12, an M. tuberculosis antigen. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vacines to prophylactically immunise mammals (especially
tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAX19460 and AAX19083 to AAX39225 are used in the exemplification of the present invention
                                                                                                                                                                                                   50
                                                                                                                                                                                                                      11 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGGATTCGCCATTCCGATC 70
                                                                                                                                                                                                   ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ь
В
                                                                   Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dillon
                                                                                                                                                                                                                                                                                                                                                                               M. tuberculosis DNA encoding a partial antigen TbRa12.
                                                                                                    447
30
00
00
                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcneill PD,
                                                                                                                                                                                                                                                                                                                                                                                                    antigen; vaccine; tuberculosis; AIDS;
                                                                                                                                                                                                                                                                    descadescandescancescadescadans 100
                                                                                                                                                                                                                                                GlyGlnAlaMetAlaileAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "TbRal2"
/partial
/note= "No start codon"
                                                                                                                                                                              (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                               acquired immunodeficiency disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 162; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
11. .409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Houghton RL,
                                                                                                                                                                               US-09-684-215B-17 (1-30) x AAZ19252
                                                                                                                                                                                                                                                                                                               ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0158338P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-2000; 2000WO-US028095
                                                                                                 8.66e-15
148.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                              AAS03780 standard; DNA; 447
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-290576/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skeiky Y, Reed S,
                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAU01889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200124820-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-1999;
07-OCT-1999;
                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                        29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-2001
                                                                                                                                                                                                   Н
                                                                                                                                                                                                                                                                  7.1
                                                                                                                                                                                                                                                                                                                                    AAS03780;
                                                                                                                                                                                                                                                21
                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                      TbRa12;
                                                                                                     ..
No.:
                                                                                                                                                                                                                                                                                          RESULT 13
AAS03780
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                88888888
                                                                                                                                                                                                    8
                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                ð
```

```
The invention relates to a recombinant nucleic acid molecule encoding a diagion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynuclectide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                        70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; immunity; diagnostic agent; gene therapy; Ral2 antigen; gene;
                                                                                                                                                                                                                                                     1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                              Seguence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis Ral2 antigen encoding DNA
                                                                   4 W O O O O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                          71 GGGCAGGCGATGGCGATCGCGGGCCAGATC 100
                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
```

```
Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a subject.
polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, M15, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis Ral2 (C-terminus of MTB32A; RA35FL) antigen encoding DNA
                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                               7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium species MTB32A C-terminal peptide encoding cDNA, MTBRal2
                                                                                                                                                                                                                                                                                                                                                     11 AcGGCCCCCCCCCCCCATACTTCCCACTCCCCAGGGTGGGCAGGGATCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                     1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusion protein; antigen; serological sensitivity; immune resp
tuberculosis; infection; vaccine; MTB32A; Ra32FL; MTBRa12; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11. .409
/*tag= a /*tag= a //product= "Ra35 protein fragment"
/note= "CDS does not include start codon"
/partial
                                                                                                                                                    Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;
                                                                                                                                                                                                 4 % 0 0 0 0 0 0 C
                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCAGGCGATGCCGGGCCAGATC 100
                                                                                                                                                                                                                                                                                                                                                                                                21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                        US-09-684-215B-17 (1-30) x AAD47080 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 99; 136pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD28339 standard; cDNA; 447 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky Y, Reed S, Alderson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-2000; 2000US-00597796.
01-FEB-2001; 2001US-0265737P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUN-2001; 2001WO-US019959
                                                                                                                                                                                              8.66e-15
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-147798/19.
P-PSDB; AAE17569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200198460-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-2002
                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD28339;
                                                                                                                                                                                                                                                         Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                                                g
    à
```

```
The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprising such fusion proteins. The present invention particularly relates to mucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase include two or more individual M. tuberculosis antigens which increase the eschoglocial sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for abliciting an immune response in a mammal, e.g., human, useful and the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium infection. The fusion proteins and the molycobacterium, in vitro and in vivo assays for detecting humoral artibodies or call-mediated immunity against M. tuberculosis, for the diagnosis to generate or elicit a protective immune response in a parient and for raising anti-M. tuberculosis antibodies in a non-human contains of the invention are also used as vaccines MTB32A, fusion proteins of the invention are useful as in vivo diagnostic agents for animal sequence of the invention are useful as in vivo diagnostic agents when any arms and for raising anti-M. The present sequence is Mycobacterium species for intradermal skin test. The present sequence is Mycobacterium species and any arms are useful as in vivo diagnostic adminestration arms and any arms 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ral2; serine protease antigen; WTB32A; Mycobacterium tuberculosis;
vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
immunogen; cytokine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGCGGGCAGGGATTCGCCATTCCGATC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence encoding Ral2-mammaglobin fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "Ral2-mammaglobin fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-17 (1-30) x AAD28339 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-OCT-2000; 2000WO-US027652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.66e-15
148.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL40772 standard; DNA; 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200125401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA, MTBRal2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-2003
03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL40772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             $$$$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

for diagnosing, for use in

```
The present invention describes polymucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The ancer that is diagnosed or treated is particularly prostate cancer. (I) and (III) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (III) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAAH933357 to AAH93344 and AAMO1115 to AAMO1318 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 Aceeccecerccearaacriccaecrerccaeereeereeecaeeaarrceccarrccearc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProI
                                                                                                         Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; ss; cytostatic; immunostimulant; tumour,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human /M. tuberculosis Ra12 fusion protein RA12-P510S-C cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                           New polynucleotide encoding a prostate-specific protein, monitoring and treating prostate cancer in a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-215B-17 (1-30) x AAH93896 (1-675)
                                                                                                                                                                                                                                                                                                                             Claim 8; Page 492-493; 543pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВÞ
                                                                                                         Dillon DC, Mitcham JL, MD, Fanger GR, Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
Microbacterium; tuberculosis.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS64132 standard; cDNA; 675
                     14-JAN-2000; 2000US-00483672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.45e-14
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2002 (first entry)
                                                                                              Xu J, Dille.
Kalos MD, Fanger Gk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide and am
the present invention
                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                WPI; 2001-425873/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200173032-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS64132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric.
                                                                                                                                                                                                                                                                                       vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS64132
ID AAS6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                    The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 Kbaic and C-terminal fragment of serine protease antigen MTB32A of equence.

Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence represents the DNA encoding the Ral2. mammaglobin fusion protein. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAla1leProlle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 84
                                                                                                                                                                                              Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 672 BP; 160 A; 185 C; 187 G; 140 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   672
000
000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 édecadocearidecearicecedeceacare 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215B-17 (1-30) x AAL40772 (1-672)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ra12-P510S-C construct cDNA sequence.
                                                                                                                                                                                                                                                                                       Disclosure; Fig 5; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-2001; 2001WO-US001574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH93896 standard; cDNA; 675
99US-0158585P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44e-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                    Skeiky Y, Guderian J;
                                          (CORI-) CORIXA CORP.
                                                                                                                                 WPI; 2001-266299/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                        P-PSDB; AA022141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WC200151633-A2.
07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH93896;
```

RESULT 17

ઠ ద ò 20 81

675 000 000 000

Length:
Matches:
Conservative:
Mismatches:
Indels:

Gaps:

```
phosphatase; PAP; prostate specific membrane antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                           HURAL J.
                                                    US2002192763-A1
prostatic acid
PSMA; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                        19-DEC-2002
                                                                                                                                                                                                                                                                                                                                          (HURA/)
(MCNE/)
(HOUG/)
(DBAS/)
(FOYT/)
                                                                                                                                                                                                    (JIAN/)
(KALO/)
(FANG/)
(RETT/)
                                                                                                                                                                                                                                                                           (LISX/)
                                                                                                                                                                     (DILL/)
(MITC/)
(HARL/)
                                                                                                                                                                                                                                                                                                           (SKEI/)
(HEPL/)
                                                                                                                                                                                                                                                                    VEDV/)
                                                                                                                                                                                                                                                                                                                                  HEND/)
 The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antignic epitopes derived from them) and antignn-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The prostate specific polynucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                              human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA;
                                                                                                                                                                      Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                     Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
0
0
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prostate cancer therapy associated cDNA #647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGCAGGCGATGGCGATCGCGGGCCAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyGlnAlaMetAlaIleAlaGlyGlnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-17 (1-30) x AAS64132 (1-675)
                                                                                                                                                                                                                                                                               Example 17; Page 532; 579pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACA59940 standard; cDNA; 675 BP
                            09-MAY-2000; 2000US-00568100.
13-MAY-2000; 2000US-00570737.
13-JUN-2000; 2000US-005737.
27-JUN-2000; 2000US-0055783.
29-MUG-2000; 2000US-00551236.
06-SEP-2000; 2000US-00551236.
06-CT-2000; 2000US-00651236.
10-OCT-2000; 2000US-0065166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.45e-14
148.00
100.00%
100.00%
27-MAR-2001; 2001WO-US009919
                      2000US-00536857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                WPI; 2001-639232/73
                                                                                                                                                   (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                            P-PSDB; AAU69899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACA59940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACA59940
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SZZZSZSZ
```

```
The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPIO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer form part of the printed specification, but was obtained in electronic form part directly from the US patent office at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotide, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalos MD;
Carter D;
Hural J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retrer MW, Stolk JA, Day CH, Vedvick TS, Li SX, Mang A, Skelky YAW, Hepler WT, Henderson RA, Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        675
30
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prostate specific protein and its encoding treatment and diagnosis of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 17; SEQ ID NO 822; 85pp; English.
                                    04-OCT-1999; 99US-0157455F.
04-OCT-2000; 2000US-00679272.
28-MAR-2001; 2001US-00822827.
29-JUN-2001; 2001US-00895793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1,45e-14
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ς
.
                                                                                                                                                                                                                                                                                                                                                                                                           LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C
FOY T M.
                                                                                                                               XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S I
JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                           T S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-245062/25.
                                                                                                                                                                                                                                                                                                               STOLK J A.
DAY C H.
VEDVICK T S
CARTER D.
```

```
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                    WPI; 2002-255649/30.
                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200289747-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                    ACC95667;
                                                                                                                                                                                                                                                                                       21
(HEPL/)
(HEND/)
                                                                                                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                                                                                                      RESULT 21
                                                                                                                                                                                                                                                                                                                               ACC95667
                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                       ઠે
                                  22 ACGGCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 81
                      1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                       Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; gene therapy; gene; ss.
                                                                                                                                                        Ra12- P510S-C construct cDNA sequence SEQ ID NO 822.
                                                   GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
        US-09-684-215B-17 (1-30) x ACAS9940 (1-675)
                                                                                                   ABL95503 standard; cDNA; 675 BP.
                                                                                                                                                                                                                                                                       25-FEB-1997; 97US-00806099.
01-AUG-1997; 97US-000904804.
10-FEB-1998; 98US-00030556.
25-FEB-1998; 98US-0001556.
23-SEP-1998; 98US-00115453.
23-SEP-1998; 99US-00159812.
15-JAN-1999; 99US-00232142.
12-NOV-1999; 99US-00288946.
13-JUL-1999; 99US-00439313.
18-NOV-1999; 99US-00439313.
12-NAR-2000; 2000US-00443686.
14-JAN-2000; 2000US-0058687.
27-MAR-2000; 2000US-0058687.
27-JUN-2000; 2000US-0058687.
13-JUN-2000; 2000US-00583793.
13-JUN-2000; 2000US-00583793.
13-JUN-2000; 2000US-00583793.
10-AUG-2000; 2000US-00593793.
10-AUG-2000; 2000US-00593793.
10-AUG-2000; 2000US-00593793.
                                                                                                                                                                                                                                                           12-JAN-2001; 2001US-00759143
                                                                                                                                                                                           Mycobacterium tuberculosis.
Homo sapiens.
Chimeric.
                                                                                                                                 (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S L.
JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LI S X.
WANG A.
SKEIKY Y A W.
                                                                                                                                                                                                                            US2002022248-A1
                                                                                                                                29-AUG-2003
19-JUL-2002
                                                                                                                                                                                                                                           21-FEB-2002
                                                                                                                  ABL95503;
                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (XUJJ/)
(DILL/)
(MITC/)
(HARL/)
(JIAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FANG/)
                                                                                    RESULT 20
                                                                                           d
                                                    à
```

```
The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the disgnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention. (Updated on 29-AUG-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
Kalos MD, Fanger GR, Retter MM, Stolk JA, Day CK, Vedvick TS;
Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
Momenil PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
Deng T;
  Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic, gene therapy, prostate-specific protein; PSP; human; immune response; prostate cancer; ss.
                                                                                                                                                     New prostate-specific polynuclectides for diagnosing and treatir diseases, in particular prostate cancer, and as markers for the progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            675
000
000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate tumour specific cDNA sequence SEQ ID 822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                   Example 17; SEQ ID NO 822; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-17 (1-30) x ABL95503 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACC95667 standard; cDNA; 675 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2001; 2001US-00852911.
29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2002; 2002WO-US014753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.45e-14
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-AUG-2003 (first entry)
```

```
Alignment Scores:
Pred. No.:
Score:
The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to illustrate the invention
                               New prostate-specific proteins and genes, useful in gene therapy, particularly for stimulating an immune response in a patient, or treating prostate cancer in a patient, as well as for diagnosing prostate cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                          50
                                                                                                                                                                                                                                                                                                                                                                      22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCGGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; prostate specific cDNA; cytostatic; immunostimulant; gene therapy; cell therapy; vaccine; T-cell epitope; class I major histocompatibility complex allele; MHC; prostate cancer; tumour; antigen presenting cell; gene; fusion protein.
                                                                                                                                                                                                                                                                                                                                                          ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate specific protein P510S-RA12 construct C cDNA.
                                                                                                                                                                                                        Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                               675
30
0
0
0
                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                         GGCAGGCGATGCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                              Example 17; Page 601-602; 691pp; English.
                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                   US-09-684-215B-17 (1-30) x ACC95667 (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB14272 standard; cDNA; 675 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-00806099.
97US-00904804.
98US-00030607.
98US-00115453.
98US-00115453.
99US-00158946.
99US-00352616.
99US-00433313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002US-00294025
                                                                                                                                                                                                                                        1.45e-14
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2003 (first entry)
           WPI; 2003-167130/16.
                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003185830-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-2002;
                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1997
09-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1999
18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB14272;
                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric
                                                                                                                                                                                                                                                                                               Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 22
```

à d ò

```
The invention relates to an isolated polypeptide comprising no more than the invention relates to an isolated polypeptide comprising on the invention relates to an isolated plant of the contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) T-cell epitopes for 3 class I major histocompatibility complex (MHC) and the proteins and peptides, expression vectors, a host cell comparing the proteins and peptides, expression vectors, a host cell comparing the protein and peptides, expression vectors, a host cell craneformed with the vector, an isolated antibody for antiple bridge containing agent that binds to the protein or peptide, detecting a patient comprising as Abalis5s, detecting the amount of polypeptide that binds to the agent and comparing the amount of cancer), a fusion protein cappearing the peptides or proteins, stimulating or expanding T cells of a predetermined cut-cell applied for a predetermined cut-cell experience or a protein comprising the peptides or protein comprising the peptides or protein comprising the peptides or protein comprising or expanding T cells cancer in a patient and treating prostate cancer in a patient with the peptides or antigen presenting cells that express the concursing contacting cells that express the peptides or that hybridies to nucleic and encoding them), is used to detect the contacting cells are the patient. The peptides (or an oligonucleotic contact and apatient may apatient. The peptides, mucleic acids encoding, or antigen presenting cells expressing the nucleic acids and administering cells expressing the nucleic acids and administering cells expressing the nucleic acids, are used to stimulate or expand T cells specific for a tumour protein. The peptides or treat the present cancer in a patient. The peptides (or an oligonucleon or antigen protein cancer in a patient. The present expense of cancer in a 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?Doc1D=20030185830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 17; Page; 101pp; English.
2000US-00593793
2000US-00605783
2000US-00651215
2000US-00657279
2000US-00679426
2000US-00679426
2000US-00679426
                                                                                                                                                                                                                                                                                                                                2001US-00759143.
2001US-00780669.
2001US-00852911.
2001US-00895814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-2001; 2001US-00012896
09-MAY-2002; 2002US-00144678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu J, Stolk JA, Kalos MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-756193/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ADB14275
                                                                                     09-AUG-2000; 2
29-AUG-2000; 2
06-SEP-2000; 2
                                                                                                                                                                                                            02-OCT-2000; 2
10-OCT-2000; 2
09-NOV-2000; 2
        13-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2001;
29-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer
```

RESULT 23

8 d ઠ

```
The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 (Sta C-terminal fragament of serine protease antigen MTB2A of a 14 Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.
                                                                                                                   25 ACGGCCGCGTCCCATAACTTCCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGATC 84
                                                                                   ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence encoding Ra12-DPPD fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
4. 1696
/*t.og6 //*t.pepp fusion protein"
/product= "Ral2-DPPD fusion protein"
                                                                                                                                                                                                              85 dedecadeceargecearcecedeceagare 114
                                                                                                                                                                     21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                           US-09-684-215B-17 (1-30) x AAZ20206 (1-702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 3; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0158585P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-OCT-2000; 2000WO-US027652
                                                                                                                                                                                                                                                                                                 AAL40770 standard; DNA; 702
                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeiky Y, Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-266299/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AA022139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200125401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2001
                                                                                      н
                                                                                                                                                                                                                                                                                                                                          AAL40770;
                                                                                                                                                                                                                                                      RESULT 24
                                                                                                                                                                                                                                                                               AAL4077
                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This DNA sequence includes a coding region for a recombinant Mycobacterium tuberculosis bi-antigen fusion protein (see AAY32071), termed Mb24, composed of the antigens Ral2 and DPPD. The DNA is useful for the recombinant production of the fusion protein. Coding sequences for the antigens were modified by PCR in ord; to facilitate their fusion and subsequent expression of the fusion protein. and then ligated. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polymuclectides encoding them are useful as vaccines for preventing tuberculosis claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective
                                                                                                                                                   1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                              New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuberculosis, antigen, fusion protein; Mtb24; Ral2; DPPD; diagnosis; therapy; vaccine; immunogen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunogens than mixtures of the individual protein components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis antigen fusion protein Mtb24 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30
30
0
0
      0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                  GGCAGGCGATGGCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                    GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto A;
                                                                                                          (1-675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Fig 13A-B; 83pp; English.
                                                                                                          US-09-684-215B-17 (1-30) x ADB14272
                                                                                                                                                                                                                                                                                                                                                                 AAZ20206 standard; DNA; 702 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-00056556.
98US-00223040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.52e-14
148.00
100.00%
100.00%
  100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky YAW, Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-601610/51.
P-PSDB; AAY32071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-APR-1998;
30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9951748-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-OCT-1999
                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                            AAZ20206;
```

Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;

```
01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK39769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "No start or stop codon"
/transl_except= (pos:1. 2, as:pro) /transl_except=
(pos:39 - 41, as:Aaa) /transl_except= (pos:321. .323,
aa:Xaa) /transl_except= (pos:339. .341, aa:Xaa)
/transl_except= (pos:450. .452, aa:Xaa) /transl_except=
(pos:621. .623, aa:Xaa)
/note= "No start or stop codon. Xaa= In frame stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       frans1_except= (pos:694. .696, aa.Xaa)
note= "No start or stop codon. Xaa= In frame stop codon"
2. .702
*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /partial
/note= "No start or stop codon"
/transl_except= (pos:263..265, aa:Xaa) /transl_except=
(pos:353..355, aa:Xaa) /transl_except= (pos:395..397,
aa:Xaa) /transl_except= (pos:470..472, aa:Xaa)
/transl_except= (pos:701..702, aa:Ser)
/note= "This codon has an apparent 1 nucleotide deletion
which alters the reading frame. Xaa= In frame stop codon"
                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                              Acedocecocreania Actitica de transcriete con esta de descriete de 1800 de 1800
                                                                                                                                                                                                                                                                                                                      ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProlle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein; tuberculosis; Mycobacterium tuberculosis; tuberculostatic; immunogen; vaccine; Ra12-DPPD; Mtb24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding antigenic fusion protein Ral2-DPPD (Mtb24)
                                                    707
300
000
000
                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCAGGCGATGGCGATCGCGGGCCAGATC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyGlnAlaMetAlaileAlaGlyGlnile 30
                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                              (1-702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag= c
product= "Mtb24 #3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product= "Mtb24 #2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag= a
product= "Mtb24 #1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .702
                                                                                                                                                                                                                                                              US-09-684-215B-17 (1-30) x AAL40770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00287849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-00818112
                                                       1.52e-14
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK14140 standard; DNA; 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      partial
                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002009459-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-2003
08-MAY-2002
                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                      ч
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK14140;
                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric
                                                                 ..
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK14140
ABX11
ABX
                                                                                                                                                                                                                                                                                                                                                                              음
                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

```
The invention relates to a purified polypeptide which induces an immune response of Mycbacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis; prection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents DNA encoding an M. tuberculosis tuberculosis, protein of the invention. This polymucleotide encodes 3 different proteins, each in a different reading frame. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fusion proteins of Mycobacterium tuberculosis antigens, useful for diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 ACGGCCGCCTCCGATAACTTCCAGCTGTCCCAGGTGGGCCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lung tumour; cancer; T cell; immune response stimulator; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding lung tumour protein P801P ORF5 and Ra12 fusion protein.
                                                                                                                                                                                                                                                                                                                         Ä
                                                                                                                                                                                                                                                                                                                         Campos-Neto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                      Reed SG, Skeiky YA, Dillon DC, Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 GGCAGGCGATGGCGATCGCGGGCCAGATC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215B-17 (1-30) x ABK14140 (1-702)
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-171134/22.
P-PSDB; AAU74600, AAU76541, AAU76542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example, Fig 13; 62pp; English.
97US-00942578.
98US-00025197.
98US-00056556.
98US-00223040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK39769 standard; cDNA; 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.52e-14
148.00
100.00%
100.00%
                                                                                                                                          (REED/) REED S G.
(SKEI/) SKEIKY Y A.
(DILL/) DILLON D C.
(ALDE/) ALDERSON M.
(CAMP/) CAMPOS-NETO A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200204514-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                              18-FEB-1998;
07-APR-1998;
30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-2002
```

```
The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating lung cancer in a patient. The polynucleotide is also useful for treating a lung cancer in a patient. The polynucleotide is also useful for treating probe or primer to detect the level of manA encoding a tumour protein. This sequence encodes a lung tumour associated protein or protein described in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                        Mcnabb A;
                                                                                                                                                                                                                                                                                   Novel polynucleotide encoding a lung tumor polypeptide useful for stimulating and/or expanding T cells specific for a tumor protein.
                                                                                                                                                                                         Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS,
Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 822 BP; 146 A; 281 C; 270 G; 125 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             857
0000
0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                         Example 8; SEQ ID NO 1862; 223pp; English.
                                                          29-AUG-2000; 2000US-00651563.

08-SEP-2000; 2000US-0058824.

26-SEP-2000; 2000US-00671325.

06-OCT-2000; 2000US-0077419.

30-OCT-2000; 2000US-00702705.

13-DEC-2000; 2000US-0078557.
                       10-JUL-2001; 2001WO-US022058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.85e-14
148.00
100.00%
100.00%
                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                            2002-164634/21.
                                                                                                                                                                                                                                                          P-PSDB; AAU85587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
17-JAN-2002
```

Novel lung cancer polymucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer.

Switzer AP, Mcneill PD;

Wang T,

Wang A,

Fanger GR,

Bangur CS, Clapper JD;

BANGUR C S. FANGER G R. WANG A. SWITZER A P. MCNBILL P D. CLAPPER J D.

(FANG/) WANG/

(SWIT/)
(MCNE/)
(CLAP/)

WPI; 2003-352750/33. P-PSDB; ABU69562.

03-MAY-2001; 2001US-00849626 13-DEC-2000; 2000US-00736457

JS2002197669-A1 sapiens.

Synthetic.

26-DEC-2002

```
The invention relates to a polymuclectide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in the specification, or a sequence (22) mentioned in specification, or a sequence selected from any of the 14 sequences mentioned in the specification, or a sequence complement of S1, sequences that hybridise to S1, sequences having 75% preferably 0%, identity to S1, or despensate variants of S1. Also included are an isolated polymotlectide, or sequences having 15% preferably of the polymotlectide, or sequences having at least 70%, or despensate variants of S1. Also included are an isolated polymotlectide, or sequences having at least 70%, or expression or vector comprising the polymotlectide or an expression control sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that specifically binds to the polymotlectide by polymotlectide, an oliginal polymotlectide that hybridises to S1 under moderately stringent conditions, atimulating and/or expanding T cells specific for a tumour protein (comprising contacting cells, under conditions and for a time sufficient to permit the stimulation and/or expanding T cells specific for a tumour protein (comprising contacting the polymotlectide, protein or antigen-presenting cells, under conditions and for a time sufficient to proliferated T cells and thus inhibiting the development of a cancer in presenting cells that express the polymotlectide, protein or antigen presenting cells, under conditions and publication or cells isolated from a patient with the polymotlectide, protein or expension of the protein or antigen. The polymotlectide, protein an effective amount of the proliferated T cells and thus inhibiting the development of a cancer in composition for stimulating an immune response in a patient, and patient (particularly lung cancer of a cancer in patient. The protein and oligonuclectide is protein consostions, e.g. vaccines. The polymotlectide is protein compos
Sxample 8; Page; 72pp; English.
```

20

22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 81 1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle

US-09-684-215B-17 (1-30) x ABK39769 (1-822)

8 g ઠે g

Percent Similarity: Best Local Similarity:

Query Match: DB:

ACA12098 standard; cDNA; 822 BP

RESULT 27

Human lung cancer protein L801P ORF5/Ra12 fusion protein cDNA.

06-JUN-2003 (first entry)

ACA12098;

Human; lung cancer; ss; lung tumour; cytostatic; vaccine; T cell expansion; CD4; CD8; RA12; gene.

```
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-164634/21
                                                                                           Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAU85594.
                                                                                                                                                                                                                                                                                                                                                                      WO200204514-A2.
                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUL-2000;
                                                        Alignment Scores:
                                                                                                                                                                                                                                                                             21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                        17-JAN-2002
                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                     21
                                                                                                                                                                                                                                                            ABK39776;
                                                                                                                                                                                                                                                                                                                            gene; ss.
                                                                  Pred. No.:
                                                                                                                                                                                                                        RESULT 29
                                                                                                                                                                                                                                  ABK39776
   856666
                                                                                                                                                                                                     g
                                                                                                                                                                                                                                           ò
                                                                                                                                                                                     ò
                                                                                                              20
                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated polymucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polymucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                          ThralaalaseraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaileProile
                                                                                                                       ACGGCCGCCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide, useful for preparing a composition for treating inhibiting development of cancer, e.g. lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcnabb
                                                                                                                                                                                                                                                                           Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watanabe Y, Johnson JC, Retter MW;
inger GR, Vedvick TS, Bangur CS, M
 T; 0 U; 0 Other;
                           000000
                                                                                                                                                                                                                                                         therapyand diagnosis associated DNA #5.
                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                       GlyGlnAlaMetAlaileAlaGlyGlnile 30
270 G; 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; SEQID NO 1862; 82pp; English.
                                                                        Gaps:
                                                                                          (1-822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fanger GR,
                                                                                       US-09-684-215B-17 (1-30) x ACA12098
                                                                                                                                                                                                                                                                                                                                                                 30-JUN-1999; 99US-00346492.
15-OCT-1999; 99US-00419356
17-DEC-1999; 99US-004166867.
30-DEC-1999; 99US-004166867.
30-DEC-1999; 99US-004166867.
10-MRR-2000; 2000US-00519642.
22-MRR-2000; 2000US-00519642.
11-JUL-2000; 2000US-005614124.
11-JUL-2000; 2000US-0051844.
11-JUL-2000; 2000US-0051844.
11-JUL-2000; 2000US-0051842.
29-AUG-2000; 2000US-00511325.
26-SERP-2000; 2000US-00571325.
                                                                                                                                                                                                   ACA03284 standard; DNA; 822 BP.
A; 281 C;
                         1.85e~14
148.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                 10-JUL-2001; 2001US-00902941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-OCT-2000; 2000US-00702705.
13-DEC-2000; 2000US-00736457.
03-MAY-2001; 2001US-00849626.
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang T,
Carter D, Fi
146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-328427/31
                                          Percent Similarity:
Best Local Similarity:
BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Henderson RA,
Sequence 822
                                                                                                                                                                                                                                                                                             Homo sapiens
                 Alignment Scores:
                                                                                                                                                                                                                                        22-MAY-2003
                                                                                                                                                                                                                                                          cancer
                                                                                                                                                                                                                                                                                                                                21-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Durham M,
                                                                                                                                                                                                                    ACA03284;
                                                                                                                            22
                                                                                                                                             21
                                                              Query Match
                           М
Э
                                                                                                                                                                                                                                                         rung
                                                                                                                                                                                  RESULT 28
                                                                                                                                                                                                     à
                                                                                                                          g
                                                                                                                                             ò
```

```
for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polynucleotide associated with the compositions and methods for the therapy and diagnosis of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcnabb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lung tumour; cancer; T cell; immune response stimulator; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotide encoding a lung tumor polypeptide useful for stimulating and/or expanding T cells specific for a tumor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS,
Wang A, Fanger N, Switzer A, Moneill PD, Clapper JD;
                                                                                                              Sequence 822 BP; 146 A; 281 C; 270 G; 125 T; 0 U; 0 Other;
                                                                                                                                                                                                     825
0000
0000
                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCAGGCGATGCCGATCGCGGGCCAGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding Ral2S-L985P fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1877; 223pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215B-17 (1-30) x ACA03284 (1-822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK39776 standard; cDNA; 861 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-2000; 2000US-00651563.

08-SEP-2000; 2000US-00658824.

26-SEP-2000; 2000US-00671325.

06-OCT-2000; 2000US-0077419.

30-OCT-2000; 2000US-00702705.

13-DEC-2000; 2000US-00734657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUL-2001; 2001WO-US022058
                                                                                                                                                                                            1.85e-14
148.00
100.00%
100.00%
```

```
88888888888888
```

```
lung cancer in a patient. The polypeptide is useful for removing tumour cells from a biological sample. The polybucicetoide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This sequence encodes a lung tumour associated protein or protein. Fragment, described in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
```

Sequence 861 BP; 186 A; 244 C; 209 G; 222 T; 0 U; 0 Other;

```
861
30
0
0
0
       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                               21 GlydlnalaMetalailealaclyGlnile 30
                                                 Gaps:
                                                                US-09-684-215B-17 (1-30) x ABK39776 (1-861)
       1.96e-14
148.00
100.00%
100.00%
                      Percent Similarity:
Best Local Similarity:
Alignment Scores:
Pred, No.:
                                       Query Match:
DB:
                  Score:
                                                                                                                ઠે
                                                                                 ò
```

ACA12105 standard; cDNA; 861 BP ACA12105; RESULT 30

Human, lung cancer; ss, lung tumour; cytostatic, vaccine; T cell expansion; CD4; CD8; RA12; gene. Human Ral2S-L985P fusion protein cDNA. 06-JUN-2003 (first entry)

03-MAY-2001; 2001US-00849626. US2002197669-A1. Homo sapiens. 26-DEC-2002 Synthetic.

BANGUR C S. FANGER G R. WANG A. (BANG/) (FANG/) (WANG/) (WANG/) (SWIT/) (MCNE/)

13-DEC-2000; 2000US-00736457.

Switzer AP, Mcneill PD; Wang T, Wang A, Fanger GR, Bangur CS, Clapper JD;

SWITZER A P. MCNEILL P D. CLAPPER J D.

(CLAP/)

WPI; 2003-352750/33. P-PSDB; ABU69569.

Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer.

Example 10; Page; 72pp; English

The invention relates to a polynuclectide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in the specification or a sequence selected from any of the 14 sequences mentioned in the specification.

The specification or a sequence consisting of at least 20 contiguous residues of \$1, sequences that hybridise to \$1, sequences having \$2\$, preferably \$0\$, identity to \$1, or degenerate variants of \$1. Also included are an isolated polypeptide (comprising a sequence (83) selected from any one of the 4 amino acid sequences mentioned in the specification, a sequence encoded by the polynuclectide, or expression vector comprising the polynuclectide operably linked to an expression vector comprising the polynuclectide operably linked to an expression vector comprising the polynuclectide operably linked to an expression vector comprising the polynuclectide operably linked to an expression ording on the polynuclectide operably linked to an expression ording of the polynuclectide operably linked to an expression ording on the polynuclectide operably linked to an impact of the polynuclectide operably linked to an expression ordition, such the polynuclectide, protein conditions, stimulation and/or expanding the polynuclectide, protein or antigen protein (comprising cells, under conditions and for a time sufficient to permit the stimulation and/or expandion of T cells and inhibiting the development of a cancer in a presenting cells that express the polynuclectide, such that T cells approximated from a patient (by incubating the presence of a cancer in the patient. The polynuclectide, such that T cells are the patient with the polynuclectide, such that T and or the patient. The polynuclectide is not the patient (particularly lung cancer). The composition is useful for decenning the presence of a cancer in a patient (particularly lung cancer). The present sequence encodes a fusion of the polynuclectide is useful for isolating a full or head of the print of a sequence encodes a tr segdata.uspto.gov/sequence.html?DocId=20020197669

Sequence 861 BP; 186 A; 244 C; 209 G; 222 T; 0 U; 0 Other;

861 0000 0000 Length:
Matches:
Conservative:
Mismatches: 1.96e-14 148.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB:

US-09-684-215B-17 (1-30) x ACA12105 (1-861)

81 22 ACGGCCGCCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlalleProI GlyGlnAlaMetAlaIleAlaGlyGlnIle 30 21 g ò δ

deccadectarectartectedectatre

82

April 29, 2004, 23:03:07 9 secs completed: A Search con Job time